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-Q=CQG012_1VGPFO_SPOOL/VSIOU48196/runat_28042003_151439_5581/app_query.fasta_1.327
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1 MMKILYVTATLMTAFTLASC......SLKPCMLETVNAFIVPTTR 134
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version 5.1.4_p5_4578 - 2003 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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NWAS22491 329861 bp DNA linear BCT 04-DEC-2 Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 5/7. ALI62756 ALI57959 ALI62756.2 GI:7380091
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Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher, Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T. Daviss,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Ouail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G. Complete DNA sequence of a serogroup A strain of Neisserla meningitidis 22491
                                                                                                                                                                                                                                                                   ProAsnalaArgThrGluValAlaGlnLysTleValArgHisSerLeuLysProCysMet
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
    catarrhalis genome
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                                                                 /organism="Moraxella catarrhalis"
/db_xref="taxon:480"
b 8751 c 7476 g 11208 t
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Matches:
Conservative:
Mismatches:
Indels:
  Nucleotide sequences of moraxella or
Patent: WO 00789684 A 21 28-DEC-2000
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Moraxella catarrhalis
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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Moraxella catarrhalis
Bacțeria; Proteobacteria; gamma subdivision; Moraxellaceae;
Moraxella.
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/db_xref="taxon:480"
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Matches:
Conservative:
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Patent: WO 0109331-A 1 08-FEB-2001;
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Lagace, R.E., Patterson, C. and Berg, K.L.
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Sequence 21 from Patent WO0078968.
AX067446
            AX081157 405 bp
Sequence 1 from Patent WO0109331.
AX081157
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ORPPLARSYSVASANWREHLBFFSIKVODGPLTSRLQHLKVGDDVLISKRPTGFLVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                NALMFGNLEGIPLDTGIRQEAEAGKADAWLAGLEAIARVHKKQQFLSQAFARNMMSDG
KNISFLDFEDDPSEVLTIAQCQARDWLCYIHSTALILKNGGLLEAAAEKWGGVLSDQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /BC_number="1.18.1.2"
//BC_number="1.18.1.2"
//note="NMA1442, fpr, probable ferredoxin--NADP reductase,
//note="NMA1442, fpr, probable ferredoxin--NADP reductase
(EMB:1.36319), fpr, Azotobacter vinelandii
ferredoxin--NADP reductase (EC 1.18.1.2) (257 aa), fasta
scores; E(): 0, 69.8% identity in 255 aa overlap. Similar
co.NM1664, fasta scores; E(): 1.3e-30, 34.6% identity in
257 aa overlap. Contains Pfam match to entry PF00175
oxidored_fad, Oxidoreductase FAD/NAD-binding domain"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2904. .2937
/note="Stem loop containing DNA uptake sequences: acgat gccgtctgaa gccc ttcagacgc atata"
2909. .2918
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00175 oxidored_fad,
Oxidoreductase FAD/NAD-binding domain, score 20.00,
E-value 8.4e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90% match to ATTCCCNNNNNNNGGGAAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEIQKLIAATVKPILPIRRLEHPRWGRDALRLAASISLISLADMPP<sup>.</sup>
2904. .2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative ferredoxin--NADP reductase"
/protein_id="CAB84678.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2923. .2932)
/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
          complement(922. .931)
/note="Core DNA uptake sequence: gccgtctgaa"
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/protein_id="CAR84677.1"
/db_xref="G1:7380094"
/db_xref="SPTREMBL:Q9JU90"
                                                                                                                                                                                  /note="NMA1441, len: 264 aa; unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:09JRE3"
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4159. .4320
                                                                                                                                                                                                                                     /transl_table=11
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                                                                                2094. .2888
/gene="NMA1441"
                                                                                                                                     2094. .2888
/qene="NMA1441"
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/gene="fpr"
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/gene="fpr"
3076. .3852
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4039, .4058
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/note=">= 90
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/gene="fpr"
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/note=">= 9
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        misc_feature
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//translat.ton="MNKTLSTLEVAILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVE
//translat.nrssewelt/arlaxsaekgaewenkicacvageapngltgndvmgmldpstr
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KWRGLAYPELAFEIMRLFVTDIPEDDLRDILNRTYTEAAFGTKEITPVRTLSDGIKIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFMLSPDGKMSAFQRAQMYSLQDGNIHNIAVKGMFDDCQDIVKAVQNDAAFKEKYHIG
TVNSINWGRIVAQVVYYFAGYFKATQSNDEQVSFCVPSGNFGNVCAGHIAKQMGLPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EINTLMAEVAAGKGFNLRFALDKVGGKYGFTSGKSTHADRLATIRQVYEQDQELIDPH
TADGVKVAREVREERETVVCLETALAAKFDATIREAVGDVAIPRPAALEGLENLPQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSNGPTLAFKDMAMQFLGNAFEYVLNKEGKKLNILGATSGDTGSAAEYALRGKKGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLIVATNENDVLDEFFKTGAYRPRNSAHTYVTSSPSMDISKASNFERFVFDLMDRDPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NWA1440, thrc, probable threonine synthase, len: 485 as; similar to many e.g. SW.THRC_METGL (EMBL:D14071), whichylobacillus glycogenes threonine synthase (EC 4.2.99.2) (475 as), fasts scores; E(): 0, 61.9% identity in 475 as overlap. Contains Pfam match to entry PF00291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown, contains a probable N-terminal signal seguence and an appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S_T_dehydratase, Pyridoxal-phosphate dependent enzymes"
/codon_start=1
/transl_table=11
                                                                                                                        Notes:
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /going membrane lipoprotein lipid attachment site" complement(571. .580)
/note="Core DNA uptake sequence: gccgtctgaa"
Parkhill,J.
Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00291 S_T_dehydratase, Pyridoxal-phosphate dependent enzymes, score 231.80, E-value 1e-65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NMA1439, possible lipoprotein, len: 123 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592. ,601
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                                                                                                                                                                                                                                                     1. 329861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      638. .2047
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/EC_number="4.2.99.2"
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                                                                                                                                                                                                                                                                                                                                                             /note="serogroup: A"
194. .565
                                                                                                                                                                                                                                                                                                                                                                  194. 565
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194. see
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AUTHORS
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/translation="MAAFNTQKVLSVHHWTDAYFTFTCTRDESLRFENGQFVMVGLMV
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DLNPGKHLYLLSTGTGTAPFLSTTKDPETYEQFEKTILVHGVRYKKDLAYYDRFTKEL
PEHEYLGDLVKEKLIYYPIVSREEFEHHGRLTDLMVSGKLFEDIGLPKINPQDDRAML
                                                                                                                                                                                                                                Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Elsen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Nolson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.A., Mason, T., Clecko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Nelson, K.E., Eisen, J.A., Retchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Oin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V., Pappuoli, R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:L36319 PID:540280 percent identity: 86.05; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
  of 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="NMB1043"
/note="hypothetical protein; identified by Glimmer2;
putative"
Neisseria meningitidis serogroup B strain MC58 section 97
                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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20175755
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/gene="NMB1044"
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                                                                                                                  Neisseria meningitidis MC58.
Neisseria meningitidis MC58
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112. .318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                     GI:7226282
                                                                                                                                                                                                               (bases 1 to 11489)
                   the complete genome.
AE002455 AE002098
AE002455.1 GI:722628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .11489
                                                                                                                                                                                           Neisseria
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DEFINITION
                                          ACCESSION
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KEYWORDS
                                                                                                                                           ORGANISM
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JOURNAL
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                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                 Arpase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR Arpase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR (EMBI:Lil292), copA, Enterococcus hiree copper/potassium-transporting Arpase A (EC 3.6.1.36) (727 aa), fasta scores; E(): 0, 34.0% identity in 744 aa overlap. Similar to NMA1539, fasta scores; E(): 0, 34.4% identity in 735 aa overlap. Contains hydrophobic, probable membrane-spanning regions. Contains two Pfam matches to entry PF00122 E1-E2_Arpase, E1-E2_Arpases and PS00154
                                                                                                                                                                                                     /translation="MIYKKNCPNKKCYAENKMKRMVFIENGCSATVIHRTGIWKKIIH
IDIIIPFIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT 25-MAY-2000
                      unknown, lies within a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative P-type cation-transporting ATPase"
/protein_1d="CAB84680.1"
/db_xref="GI:7380097"
/db_xref="SPTREMBL:Q9JU88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ATCGTCAAAATGGCGGTAGAAAGCCAATGCCGTGCGGAATTGAACAAAGGCAGGGAATGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 CGTTTGACCGCGCTGGCGATGAGTGCCGAAAAACAGGCGGAATGGGAAAACAAGATTTGC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AlaSerThrProGluSer-----AsnProLysAsnSerSerAlaAsnLeuThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp
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28
29
58
6
                                                                                                             /product-"hypothetical protein NMA1443"
/protein_id-"ch884679.1"
/db_xref="G1:7380096"
/db_xref="SPTREMBL:09JU89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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                                       of unusually low GC content" /codon_start=1
                   /note="NMA1443, len: 53 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                             /gene="NMA1444"
complement(4509. .6980)
/gene="NMA1444"
                                                                                                                                                                                                                                                              complement(4509. .6980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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23.148
17.468
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 TGC 544
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TPLFRRTGKGMVLTRAGEILLPEAESLLQYKHKLEHFAKTLAGDYSEETSLGIIHPID
SAKIVALTDNIGGTARKTRHIQYGMSGEILSRIQHKTLHGGFILGRAAQRGIRSVFL
QNLTYALICOPSQYPHLTRSLPQSLQECWNEMSGVSGSRKHHAGFWRSNRLSPKKQI
LCDYQTIDLVAGGIGVAMYPGNKAEAAAKEGAGVAIIESCRHSMPLNFIYAEEYED
NPHYSLLLECIEKWWQWQAVQPPVYSDN"
COMPLEMENT (7718. .8683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSYTQLTQGERYHIQYLSRHCTVTEIAKQLNRHKSTISREIRRH
RTGGQVZAERAGNGSGTIRGRREQPYKLDSQLIQHIDTLIRRKLSPEDVCATLCKHH
QITLHHSTIYRYLGONSSNGSTLMGHLRICSRPYRRNGSGWTRGKYPHNYGIENRPA
IVDQKSRIGDWEADTIVGKGQKSALLTLVERVTRYTIICKLDSLKAEDTARAAVRALK
ATKDRYHTITHUNGREPYQHTRITKALKAETYRCRPYHSWEKGLNENTRDH
QTDFRNISDREIRRVGDELMHRPRKTLGYETPSVLENLFQPLIH"

COMPLEMENT (8805..10715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATRIVELDRGILRSYPGSFSKYSEKKAQELAVEAEHNRLFDKFHAQEEAWIRKGIEA
RRTRREGRYRRLEELRRQRAERRNVGGVNFKLDSGEKSGKITALEERASFAYGGKVI
RNFSALLQRGDKIGLIGPNGIGKTFEKLILGELQPTGRIRIGSKQEVAYFDGFRS
ALNENDTYFYLLGGONYVEVGGKKHHVMSYLEDFLFHPARAQSPVSSLSGGENRKLI
LAKLFTRPANILVLDEPTNDLDIDTQELLEDLLRDYQGTVFLVSHDRMFLDNVITQSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MNILSVENASFAIGHVALLDKTSFQLDSGEKVGLIGRNGACKSS
FLKILAGLQKLDDGQIIVQNNLKIVYVPQESFFDKDATVFDTVAEGLGEIRDLLRRYH
HVSHELENGSSEALLKELNELQLEIEAKDGWKLDAAVKQTLGELGLPENEKIGNLSGG
                             PID:148255
                                                                                                                                                                                                                                                       /translation="MDAVQLKSFVAVAHEGNLTQAAKRLFLSQPAVSAQIKALEEYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKKRVALAQAWVQKPDVLLLDEPTNHLDIDAIIWLENLLKAFEGSLVVITHDRRFLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L42023 PID:1007269 PID:1221430 PID:1205538 SP:Q57242 percent identity: 69.46; identified by sequence similarity; putative"
                             SP:P23841 GB:X63976 PID:14825948.44; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:L27157 PID:451858 percent identity: 62.86; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ABC transporter, ATP-binding protein,"
/protein_id="AAF41449.1"
/db_xref="C1:7226291"
                                                                                                                                   /transl_table=11
/product="transcriptional regulator, putative"
/protein_id="AAF41447.1"
/db_xref="G1:7226289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111489
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transposase, IS30
/protein_id="AAF41448.1"
/db_xref="G1:7226290"
                             /note="similar to GB:M13687
PID:41595 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
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/gene="NMB1051"
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                                                                                    putative"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="NMB1050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="NMB1050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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Best Local Similarity:
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TVNSINWGRIVAQVVYYFAGYFNATSSNDETVSCVPSGNFGNVCAGHIAKQMGLPIR
KILVATNENDVLDEFFKTAGYRPRNSAHTYVTSSPSMDISKASNFERFVFDLMDRDPA
RINTLWAASVAAGKGPDLRFALDKVGGKYGFTSGKSTHADRLATIKOYSCDOELIDPH
TADGVKVAREVREGGEMVVCLETALAAKFDATIREAVGDAAIPRPAALEGLENLPQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAF41445.1"
/db_xref="G1:7226297"
/translation="WHXTLGILPVAILLGGCAAGGGNTFGSLDGGTGMGGSTVKMAVG
SQCRAELDKRSEWRLTALAMSAEKQAEWENKICACVAQEAPERMTGNDVMQMLAPSTR
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FTSSWGTYIVPASIAKRPIPGGAVLTAVLCIIAGLWGYPMDLAIWQPVLSVALVVGVY
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FAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLEHFKSLG"
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NALWEGNLEGIPLDAQIRQEAGKSDAWLAGLEATARVHKRQFLSQAFARNAMSDG
KNISFLDFEDDPSEVLITAGOCARDMLCYIHSTALILKNGGLLEAAAFKWGGVLSDQP
AETGKLIAATVKPLLETRREHPRWGRDALRLAASISLISLADMPP"
complement (2515. .3924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P23669 GB:X56037 PID:580784
PID:580991 percent identity: 71.31; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MKYISTRGETAHKPFSEVLLMGLAPDGGLMLPEHYPQIGRETLD
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ALSNGPTLAFKDMAMQFLGNAFEYVLNKEGKKLNILGATSGDTGSAAEYALRGKKGVN
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                                                                                                                                                                                                                                                                                    /translation="MTLPMQETRFSILLDELAAKQEAAIAPHLLADGTKVWIRKAGRH
                                                                                    'note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAF41443.1"
/db_xref="G1:7226285"
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/transl_table=11
/product="hypothetical protein"
/protein_id="AAF41446.1"
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/db_xref="G1:7226286"
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/gene="NMB1047"
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/gene="NMB1047"
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/gene="NMB1049"
6345. .7259
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transl_table=11
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Homo sapiens DNA, clone:CMB9-99M9.
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79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
                                                                                                                                                                                                                            4137 GCTTGCGTCGCCCAAGAAGCACCGGAACGATGACCGCCAACGATGTG---ATGCAGATG
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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/db_xref="taxon:487"
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Best Local Similarity:
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E 2 (bases 1 to 68466);
S Hattori,M., Ishli,K.; Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakakl,Y.
Direct submission
L birect submission
L submitted (08-00v-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
Japan (E-mail:hattori099) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
URL:http://mpp.gsc.riken.go.jp/, Tel:81-42-778-9923,
ON May 31, 2000 this sequence version replaced gi:6997560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP000686 68466 bp DNA linear HTG 30-MAY-2000 Homo sapiens chromosome 11 clone CMB9-99M9 map 11q25, WORKING DRAFT SEQUENCE, 12 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                Db 163909 CTGGCTCCGTCCACGCGCAATCAGGCACTTGCCGCCCTGACGCCCAAAACGGTTTCCGCC 163850
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Hattori, M. Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 68,466 genomic DNA. of 11q25
                                                                                                                                                                                                     164026 CGTTTGACCGCGCTGCCGATGAGTGCCGAAAAACAGCGGGGAGTGGGAAAACAAGATTTGC 163967
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78
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Contact. hattoriegsc.riken.go.jp/
Conter_project Information
Center project name: Humbrafill
Center clone name: CMB9-99M9
Center clone name: CMB9-99M9
Center clone name: CMB9-99M9
Center clone name: CMB9-99M9
Consencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 66248 bases at least Q30
Consensus quality: 66248 bases at least Q30
Consensus quality: 66946 bases at least Q30
Insert size: 67366; sum-of-contigs
Quality coverage: 8.74x in Q20 bases; sum-of-contigs
                                                                                                                                                              79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
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/note="assembly_fragment"
34596. .41662
/note="assembly_fragment clone_end:T7 vector_side:left"
41763. .48030
/note="assembly_fragment"
                                                                                                               Sequence updated (26-May-139 or 1130 up in length
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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67331 68466; contig of 1136 bp in length.
Location/Qualifiers
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/note="assembly_fragment"
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'note="assembly_fragment"
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/db_xref="taxon:9606"
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61089 contig of
63744 contig of
65573 contig of
67230 contig of
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/clone="CMB9-99M9"
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AC079123 187087 bp DNA linear HTG 19-AUG-2000 Homo sapiens chromosome 11 clone RP11-507F16, WORKING DRAFT SEQUENCE, 14 unordered pieces.
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Submitted (18-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                          25971 TTAAGGCTGATGATCACAGCCACAGTAATGCAACTGTCTTCAGCAGCACATAGAACTG 26030
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Mismatches:
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Matches:
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                                                                                          Indels:
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Waterston, R.H.
                   103.50
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27.66%
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                                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                               Quality coverage: 4.81 in Q20 bases; agarose-fp Quality coverage: 4.59 in Q20 bases; sum-of-contigs
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              Sequencing vector: plasmid; 0% of reads Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: bases at least 040 Consensus quality: bases at least 030 Consensus quality: bases at least 020 Insert size: 193000; agarose-fp Insert size: 185787; sum-of-contigs
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contig of 9442 bp in length
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contig of 11501 bp in length
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gap of unknown length
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gap of unknown length
contig of 9166 bp in length
gap of unknown length
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gap of unknown leng
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/note="assembly_name:Contig12"
3000. .5703
/note="assembly_name:Contig13
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/note="assembly_name:Contig15"
17123: .26288
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47532. .61339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'clone-"RP11-507F16"
Sequencing vector: M13; 100%
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AP003327 188041 bp DNA linear PRI 08-MAR-2002
Homo sapiens genomic DNA, chromosome 11g, clone:RP11-507F16,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 182945 ACACATGGCATGGGTCAGAGTGGAATATGCAGGAAGTCCTGCCTTGACATTCCTCATCTG 183004
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mismatches:
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Matches:
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Homo sapiens
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TITLE Homo sapiens genomic DNA JOHRNAL Dublished Only in Database (2001)	ωΣ	Eukary
RENCE 2 (bases 1 to 18804). THORS Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fulyoma,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.	REFERENCE 1 AUTHORS D	Manuma 1 (bi DOE JO
TITLE Direct Submission JOURNAL Submission JOURNAL Submitted (23-FEB-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suchiro-chou, Tsurumi-tu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/,	AL RS	Unpub Unpub 2 (be DOE Jo Direct
Tel:81-45-503-7111, Fax:81-45-503-91/0) COMMENT On Mar 7, 2002 this sequence version replaced gi:13122444. FEATURES Location/Qualifiers Source 1188041 /organism="Homo sapiens"	REFERENCE 3 AUTHORS D TITLE D JOURNAL S	Genome 3 (ba DOE Ja Direct Submit
/db_xref="taxon:9606" /chromosome="11" /map="11g" /clone="RP11-507F16" ORIGIN	COMMENT D	Drive On Oct Draft www.j Finish www-sl
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Qy 2 MetLysIleLeuTyrValThralaThrLeuMetThralaPheThrLeuAka 18 ::::::::::::::::::::::::::::::::::::	Alignment Sco Pred. No.: Score:	Scores:
19	Percent Similarit; Best Local Simila: Query Match: DB:	arit mila
27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal 44	US-10-048-196-2 Qy 2 MetLys	196-2 (MetLysI
45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIlealaalaMetLys 64	::: Db 27637 TTA Qy 19	TTAAGGC
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ThrGluValAlaGlnLysIleValArgHisSe	27802	IÎI::: AAAAGAG
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Db 136678 AAT 136680 RESULT 9	Qy 85 Ala Db 27895 GCA	AlaProG [[[]]] GCACCCT
ACCIO220 ACCIO220 ACCIO290 238472 bp DNA linear PRI 23-OCT-2001 DEFINITION Homo sapiens chromosome 5 clone CTB-125B20, complete sequence. ACCESSION ACCIO290	105	ThrGluV
VERSION AC010290.7 GI:16328257 KEYWORDS HTG. SOURCE HOMO Sapiens. ORGANISM HOMO Sapiens	Qy 125 Asn 125 111 Db 27997 AAT 279	Asn 125 AAT 279

Direct Submission

To E Joint Genome Institute.

De Joint Genome Institute.

Direct Submission

Submission

Submission

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Submission

Submitted (13-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Submitted (23-OCT-2001)

Submission

Submitted (23-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Submitted (23-OCT-2001) DOE Joint Genome Institute

AWW-igi.doe.gov

Produced by DOE Joint Genome Institute

AWW-igi.doe.gov

Submission

Submitted (23-OCT-2001)

Submission

Submitted (24-OCT-2001)

Submission

Submitted (24-OCT-2001)

Submission

Submitted (24-OCT-2001)

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Submission ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; malia; Eutheria; Primates; Catarrhini; Hominidae; Homo. bases 1 to 238472)
Joint Genome Institute and Stanford Human Genome Center. ect Submission TICCTITITACACTAGTAACCCACCAAGAGAATGTTCAITITACACCCTT 27996 GGCATGGGTCAGAGTGGGAATATGCAGGAAGTCCTGCCTTGACATTCCTCATCTG 27756 TACCAG-------ACGACCATACTGTTTCGGGGGAAACATGCCAGC 27801 GlualaValSerLeuThrGluLeuThrThralaAlaIleAsnProAsnAlaArg 104 ValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrVal 124 LysAsnSerSerAlaAsnLeuThrThrSerLeuIle-----LysHisAlaVal 44 ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys 64 SerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys 84 ------SerCysAlaSerThrProGluSer 238472 339 113 52 37 5 Length:
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Mismatches:
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 10

AB058719

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE REFERENCE

AUTHORS TITLE JOURNAL

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Maruyama, N., Ichise, K., Katsube, T., Kishimoto, T., Kawase, S., Matsumura, Y., Takeuchi, Y., Sawada, T. and Utsumi, S. Identification of major wheat allergens by means of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trainiation="vRvPvPQLQPQNPSQQQPOEQVPLVQQQQFLGQQQPFPPQQPYP
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Triticum aestivum gene for alpha-gliadin mature peptide, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                          2083 TCTACTGTCTCCACGGCCACTAGTTTACCTTCTGTTGCCAGCACTCCCGCAGCTCCAAAC 2142
                                                                                                                                                                                 2143 CCTGCAAGCTCACCAGCAAACTGTGTGTGTCCAAACTCCAAAGCTCAC 2202
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alpha-gliadin mature peptide; alpha-gliadin.
Triticum aestivum (cultivar:hard red spring ICW) DNA.
Triticum aestivum
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Eur. J. Biochem. 255 (3), 739-745 (1998)
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                                                                                                                                                                                                                                                           Nagase_T., Nakayama,M., Nakajima,D., Kikuno,R. and Ohara,O.

Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

LD DNA Res. 8 (2), 85-95 (2001)

RE 21245130

Cara_O. Nagase,T. and Kikuno,R.

Sohara_O. Nagase,T. and Kikuno,R.

Direct Submission

LD Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA Rsearch Institute,
Department of Human Gene Research: 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
UKL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)

Sorganism="Homo sapiens"

// Corganism="Homo sapiens"
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ICINSSLNSSLGGAGIGVNNTPNSTPAAPSSNHPAAGGCGGSGGPGGGSAAVPKHSTV
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RLPEIKLPVNGCSDLEDSFTILQSKDLKQEPLDDPTCIDTSETSLSNQNKLFSDINLN
DQEWQELIDELANTVPEDDIQDLFNEDFEEKKEPEFSQPATETPLSQESASVKSDPSH
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NQAHTPGQAPPRFGNGYLLNPAAVTVAGSASGPVAVPSSDMSPAEQLKQMAAQQQQRA
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PAQQOIPSGSFAPSSQSQAYERNAPQDVSXNYSGDGAGGSFPGLPDGADLVDSIIKGG
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QQHPSK PQQDAEAASA EQRNHTLIMLQETVKRK LEGARSPLNGDQQNGACDGNFSPTS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               linear Pr
ortial cds.
     мвозв/19
Homo sapiens mRNA for KIAA1816 protein, partial
AB058719
                                                                                                                                    Homo sapiens brain cDNA to mRNA, clone:fh16716.
Homo sapiens
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6841 4329
/gene="KIAA1816"
/note="KIAA1 codon is not identified.
/codon_start=1
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Conservative:
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/protein_id="BAB47445.1"
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source

FEATURES

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CDS

Query Match:

Pred. No.:

Score:

BASE COUNT

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (08-A00-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Aug 8, 2002 this sequence version replaced gi:21492356.
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MCPherson, J.D. and Materston, R. H.
The sequence of Mus musculus clone
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Mus musculus chromosome UNK clone RP23-42113, WORKING DRAFT SEQUENCE, 19 unordered pieces.
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/note="N-terminal primer region for PCR" 755. 780 //note="C-terminal primer region for PCR" 246 c 119 g 155 t
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Matches:
Conservative:
Mismatches:
Indels:
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                       Chemistry: Dye-primer ET: 08 of reads
Chemistry: Dye-primer ET: 08 of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 240797 bases at least 040
Consensus quality: 242698 bases at least 030
Consensus quality: 242698 bases at least 030
Insert size: 204000; agarose-fp
Insert size: 248995; sum-of-contigs
Quality coverage: 10.08 in 020 bases; sum-of-contigs
Quality coverage: 8.91 in 020 bases; sum-of-contigs
nknown length
f 1912 bp in length
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/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-42113"
1..1085
                                                                                                               ----- Summary Statistics
                                                                                                                             Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
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99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIl 117 GTCAGAAGACAGTTCAGCTCATACACACACTTGCTGCTGAACAT 117 LysProCysMetLeuGluThrValAsnAlaPheIleValProTh 117 LysProCysMetLeuGluThrValAsnAlaPheIleValProTh 118 Lillil:::	Scores: 1.12 Length: 92.50 Matches: 29 milarity: 54.67% Conservative: 13.68% Conservative: 13.68% Indels: 29 h: 13.68% Indels: 29 196-2 (1-134) x AF223572 (1-632) AlaThrLeumetThralaPheThrLeualaSerCysalaSerThre :::
misc_feature /note="assembly_name:Contig94" misc_feature /note="assembly_name:Contig84" nisc_feature /note="assembly_name:Contig86" misc_feature /note="assembly_name:Contig86" misc_feature /note="assembly_name:Contig86" misc_feature /note="assembly_name:Contig80" misc_feature /note="assembly_name:Contig80" misc_feature /note="assembly_name:Contig90"	Alignment Scores: 1.34e+03

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The clone sequenced to the left is RP11-342I1; the clone sequenced to the right is RP11-328NB. Actual start of this clone is at base position 1 of RP11-21M10; actual end is at base position 174410 of RP11-21M10.
                                                                                                                                   Data from AC044906 and AC040995 was used to finish this clone, AC019343. Polymorphisms have been identified between AC044906, AC040995 and AC019343.
  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watersoum, a bull solution bullet Submission Submitted (01-MAR-2002) Department of Genetics, Washington Submitted (01-MAR-2002) Department of Genetics, Missouri 63108, USA On Oct 25, 2001 this sequence version replaced gi:16303526.
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-0CT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases I to 174410)
Waterston, R.H.
Direct Submission
Submitted (25-0CT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     2 (bases 1 to 174410)
Tomlinson,C., Haglund,K. and Spalding,L.
The sequence of Homo sapiens BAC clone RPI1-21M10
Unpublished (2001)
3 (bases 1 to 174410)
                                                                                                                                                                               Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                       Chordata; (Primates; (
                                                                                                                                                        Sulston, J.E. and Waterston, R.
  AC097464.3 GI:16418223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 174410)
                                                                                                                                 (bases 1 to 174410)
                                                                   Homo sapiens
Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                Homo sapiens.
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                                                                                                                                                                                                                           99063792
                                           SOURCE
ORGANISM
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AUTHORS
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1337. .4853
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The sequence of AC019343 has been incorporated into AC097464
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                                                                                                                                                                          /note="similar to EST BG571049 (NID:g13578702)"
1192. .1244
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بنه
                                          /organism="Homo sapiens"
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10737, .10809
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12826. .13022
/rpt_family="MIR"
13099. .13266
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14001, .14312
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997. ...
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RECI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catannese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACe3.6

NOTICE: This sequence may not represent the entire insert of this folore. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu ------ Summary Statistics

Center code: WUGSC

Center project name: H_NH0021M10 Drafting Center: WIBR This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

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HTG 09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 226325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sims, S.
Direct Submission
Submitted (31-70L-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mall enquiries: hundquery@sanger.ac.uk Clone requeste: clonerequest@sanger.ac.uk On Aug 11, 2002 this sequence version replaced gi:22035729.
                                                                                                                                                                                  AL845171 226325 bp DNA linear HTG 09-Al
Mus musculus chromosome 4 clone RP23-38N8, *** SEQUENCING IN
PROGRESS ***, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator; 100% of reads
Consensus quality: 218645 bases at least Q40
Consensus quality: 221861 bases at least Q30
Consensus quality: 223723 bases at least Q20
Insert size: 225125; sum-of-contigs
Insert size: 225774; 1.7% error; agarose-fp
Ouality coverage: 5.27x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10951 10950: gap of 100 bp 10951 40598: contig of 29648 bp in length 40699 40698: gap of 100 bp 40699 88025: contig of 47327 bp in length 88026 88125: gap of 100 bp 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7228: gap of 100 bp 120412: contig of 3184 bp in length 10512: gap of 100 bp 145346: contig of 24834 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5446: gap of 100 bp 164482: contig of 19036 bp in length 4882: gap of 100 bp 1772895: contig of 7713 bp in length
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20518 bp in length
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20476 bp in length
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7294 bp in length
                                                             Db 99209 GCAGTGACAGTGGCCGGTTCAGCGTCAGGGCCTGTGGCTGT 99169
                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coverage: 5.29x in Q20 bases; agarose-fp
                           67 erGluSerLysAlaLysIleSerGluThrAlaCysGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .--- Summary Statistics
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179689: contig of
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220883: cont
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HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                         house mouse.
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200308
200408
                                                                                                                                   RESULT 15
AL845171/C
                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7949. .28439
note="similar to EST BF356711 (NID:g11315785)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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1806. .27894
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6605. .27008
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                                                                              rpt_family-"AT_rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A-rich"
                                                                                                                                                            5389. .16411
rpt_family="(TG)n"
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rpt_family="MaLR"
\382. .2047?
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pt_family="(CA)n"
431, .24675
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                                                                                                                                                                                                                                                                                                                     8964. .19002
rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                   pt_family="(T)n"
715. .19863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87<u>2</u>. .19930
pt_family="MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
30318. .anfr
                                                                                                       /rpt_family="MIR"
6389, 16/11
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7080.
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rpt_family="MIR"
7949. 2842
                                                                                                                                                                                                                                                                                                                                                                                                                                                        pt_family="MIR"
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                         rpt_family="L1"
5812. .15832
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rpt_family="
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13.688
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220884 220983: gap of 100 bp
220984 226325: contig of 5342 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:01963
fragment_chain:3"
17396. 179689
/note="assembly_fragment:02198
fragment_chain:3"
179790. 200300.
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fragment_chain:3"
200408. 2200884
/note="assembly_fragment:01579
fragment_chain:3"
200984. 226335
/note="assembly_fragment:01579
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                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:01377
fragment_chain:2"
117229. 120412
/note="assembly_fragment:00099
fragment_chain:2"
120513. .145346
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                      /note="assembly_fragment:01520
fragment_chain:1"
40699. 88025
/note="assembly_fragment:02301
fragment_chain:1"
                                                                                                                                 1. .10850
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fragment_chain:1
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"assembly_fragment:02271
fragment_chain:2"
145447. .164489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145447. .164482
hotte="assembly_fragment:02356
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164583. .172295
                                                                                                                                                                                                                                                                                                  88126. .103225
/note="assembly_fragment:01187
fragment_chain:1"
103326. .117128
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a 43544 c 44968 g 67598 t
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                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
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                                                                                                                     /clone_lib="RPCI-23"
                                                                                                       /clone="RP23-38N8"
                                                                                                                                                                                             vector_side:left"
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38.10%
25.00%
13.61%
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9
                               FEATURES
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Db 114299 CTCTCGAAGCTTTTGTGGTTCACAGCAACCAGGACCTGCTTGATCTATTTTTATGAATAGC 114240

Db 114239 ATATTCTCTAGAGTCAGTGTACTGCTATTTTGAGCAATGAATCTTCTAGCCTTACAATT 114180

AlaSerThrProGluSerAsnPro-----LysAsnSerSerAlaAsnLeuThrThr 37

21

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requests: ClonerequestBanger.ac.uk

On Feb 5, 2001 this sequence version replaced gi:12655262

On Feb 5, 2001 this sequence version replaced gi:12655262

On Feb 5, 2001 this sequence version replaced gi:12655262

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL161893 62043 bp DNA linear PRI 02-FEB-2001
Human DNA sequence from clone RP11-223E19 on chromosome 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr13
RP11-223E19 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chcri.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                              114119 TCTAGCTGTGATTTATCCTATGATGTTGATGTTATGCTCCTGAGATCCAATACAAGTCAT 114060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62043)
                                      114059 TTCTCTTATCCATTTGTCTATTGGGATTTTCATGTTTTCAATGGTATGATGATGATTCTTTA 114000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
47
                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                        63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn
                                                                                                                                                                                                                                                                                                .--LysIleAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 113999 CAGTTAGTGGTTGCAATCTCAAAGGCCAAAATTTCTACCAATGACTGT-------
                                                                                                                                                   .----ThrGlyHis
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                                                                                                                                                48 -----CysGlnThrGlnLeu---------
38 SerLeuIle-----LysHisAlaValLysGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 113861 TTGGTAAATGAGGTGATTTTCCCC 113838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ThrValAsnAlaPheIleValPro 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete sequence.
AL161893
AL161893.24 GI:12666231
                                                                                                                                                                                                                                                                                                -GlnTyrTrp-
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TITLE
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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5830. 6144
/note="Aludo repeat: matches 1. 303 of consensus"
6145. 6196
/note="Aludo repeat: matches 1. 303 of consensus"
6284. 6414
/note="Aludo/PLAM repeat: matches 24. 122 of consensus"
6418. 6735
/note="Aluxb8 repeat: matches 1. 315 of consensus"
6931. 7221
/note="Aluxb8 repeat: matches 1. 292 of consensus"
7336. 7044
                                             this
                                                                                                                                                                                                                                                               504. 837
/note="LlME1 repeat: matches 5763. .6112 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551. 3709
note="L1MD3 repeat: matches 7566. 7729 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foote-"Alusq repeat: matches 1. .310 of consensus" 645. .7677 foote-"Alusque 90% conserved" 694. .8059 foote-"LLMD3 repeat: matches 7359. .7739 of consensus"
once, except for a 100 base overlap.
end of clone RP11-550P23 is at 61944 in this
true right end of clone RP11-374F3 is at 100 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18. 454
note="MER66A repeat: matches 97. .486 of consensus"
                                                                                                                                                                                                                                                                                                                           .359 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJb repeat: matches 3, .298 of consensus"
13083. .13146
/note="MER69 repeat: matches 335. .395 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                    note="MLTIB repeat: matches 1. .326 of consensus" 672. .1974
note="Alusx repeat: matches 5. .306 of consensus" 834. .3059
note="MIR repeat: matches 20. .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                               note="Alusx repeat: matches 1. .285 of consensus" 150. .1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="20 copies 2 mer aa 77% conserved"
305. .4207
octe="AluSx repeat: matches 2. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .924. .10230
'note="Aluub repeat: matches 1. .306 of consensus"
.0380. .10692
'note="Alusx repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192. .3482
note="AluSx repeat: matches 1. .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1512. 9798

Mote-"Alusx repeat: matches 3. .296 of consensus"

1924. 10230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER69 repeat: matches 2. .335 of consensus"
2786. .13082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .293. 4364
note="MIR_repeat: matches 47. 120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151. .5733
ote="HALI repeat: matches 1. .588 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note="MIR repeat: matches 35. .237 of consensus" 2474. .12785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0694. 10852
note="MIR repeat: matches 8. .186 of consensus"
1112. .11315
                                                                                                                                                                                                                                                                                                                           matches 326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER20 repeat: matches 1.
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-223E19"
                                                                                                                                                                                                                                                                                                      38. .871
note-"MLT1B repeat:
                                                                               Location/Qualifiers
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75476. 25718
/note-"MER20 repeat: matches 1. .218 of consensus" 25898. 25932
/note-"7 copies 5 mer aaaag 91% conserved" 26425. .25844
/note-"LIMD3 repeat: matches 7298. .7739 of consensus" 26933. .27243
/note-"AluSx repeat: matches 1. .311 of consensus" 77246. .27305
/note-"31 copies 2 mer at 69% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="FLAM" repeat: matches 1. .126 of consensus"
33530 .33839
/note="Alur repeat: matches 1. .309 of consensus"
34011. .3436
/note="THEIC repeat: matches 1. .371 of consensus"
34427. .35448
/note="LIPAIG repeat: matches 5155. .6157 of consensus"
35475. .35922
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27314. 27435

2740. 2809

27470. 2809

7040-"Alux repeat: matches 2. .69 of consensus"

27470. 2809

70416-"CpG island"

70416-"CpG island"

70416-"CpG island"

70416-"CpG island"

70416-"Sequence from uni-directional dGTP big dye

70616-"L2 repeat: matches 2604. 2705 of cônsénsus"

70616-"L2 repeat: matches 2546. .2709 of consensus"

28593. 28769

70616-"L2 repeat: matches 2546. .2709 of consensus"

70616-"L3 repeat: matches 1. .289 of consensus"
                                                                                /note="Alusar repeat: matches 19. .299 of consensus"
16105. .16701
/note="Limbl repeat: matches 5555. .6156 of consensus"
16702. .16997
/note="AluJo repeat: matches 1. .295 of consensus"
17451
/note="AluJo repeat: matches 1. .297 of consensus"
18666. .18789
                                                                                                                                                                                                                                                                                                                                                                           19592. .19629
/note="19 copies 2 mer aa 78% conserved"
20154. .2042. .2042.
/note="AluSc repeat: matches 5. .292 of consensus"
21501. .21634
/note="AluJb repeat: matches 1. .133 of consensus"
22047. .22097
/note="MIN repeat: matches 16. .252 of consensus"
23518. .23726
/note="MIN repeat: matches 16. .252 of consensus"
24105. .24714
/note="AluSg repeat: matches 1. .310 of consensus"
25476. .25718
                                             2224. .2511 of consensus"
repeat: matches 507. .654 of consensus"
                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2623. .2750 of consensus" 18873. .18989
//note="FLAM_C repeat: matches 1. .117 of consensus" 19209. .19507
//note="Allog repeat: matches 1. .296 of consensus" 19592. .19629
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'note="AluSx repeat: matches 1. .304 of consensus"
81171. .31491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticum.

1 (Jases 1 to 1102)
Okita,T.W., Cheesbrough,V. and Reeves,C.D.
Evolution and heterogeneity of the alpha-/beta-type and gamma-type
                                                                                                                                                                                                                                                                                                                                                                                                                                      complete
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 of consensus"
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                                                                      /note="AluSq repeat: matches 3. .294 of consensus' 38193. .38272
/note="MIR repeat: matches 67. .146 of consensus" 40216. .40395
/note="MIR repeat: matches 23. .223 of consensus" 40868. .41833
/note="CPG island"
                                    of consensus
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/note="Charlielb repeat: matches 35.
36403. .36709
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14
58
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Conservative:
Mismatches:
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J. Biol. Chem. 260 (13), 8203-8213 (1985)
85234522
                                   /note="AluSx repeat: matches 1. 36721. .37004
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/translation="MKTFPILALLAIVATTATTAVRVPVPQLQLQNPSQQQPQEQVPL
VQEQQFQGQQQPFPPQQPPPSQQPYLQLQDFPQPQLLPVPQPQPFRPQQPYPQ
PQPQYSQPQQDC1SQQQQQQQQQQQQILQQILQQQLIPRVVVLQDNNIAHGSSQV
LQESYYQLVQQLCQQLWQIPEQSRCQAIHWVHAIILHQQHHHHQQQQQQQQQQQQ
QVSFQQPQQQYPSGGGFFQPSQQNPQAQGSFQPQQLPQFEEIRNLALQTLPAMGNVXI
Sequence divergence between the classes is due to single base substitutions and to duplications or deletions within or near direct repeats. There are more than a hundred copies of the gene encoding alpha-/beta-gladin per haploid genome. Amplification or rearrangement of DNA does not occur during development, since
                                                                                                 hybridization patterns are the same, whether DNA isolated from leaves or seeds is used.
Potential polyadenylation signals are present at 1017-1022 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 AlaValLysGlnThrCysGlnThrGlnLevThrGlyHisGlnTyrTrpLysIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CAGGGATGTTGTATTGCAACAACAACATAGCGCATGGAAGCTCACAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="alpha-/beta-gliadin signal peptide"
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/note="pre-alpha-/beta-gliadin A-II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124. .936
/product="alpha-/beta-gliadin A-II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ý.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 a 327 c 181 g 229 t
upstream of PstI site; chromosome
                                                                                                                                                                                                  1. .1102
/organlsm="Triticum aestivum"
/db_xref="taxon:4565"
<1. .1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
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/db_xref="G1:170712"
                                                                                                                                                                                                                                                                               /product-"gliadin mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-048-196-2 (1-134) x WHTGLIABA (1-1102)
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CysMetLeuGluThrValAsnAla 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPYCTIAPFGIFGTN"
                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.63
89.50
37.84%
24.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                             1074-1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
123 bp u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
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Ø

Leishmania major. Leishmania major

ORGANISM

SOURCE

REFERENCE AUTHORS 98146435

PUBMEC REFERENCE

JOURNAL TITLE

TITLE JOURNAL

AUTHORS

Notes

COMMENT

AL359778.1

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 18

g

LMFL163/c

LOCUS

```
/product="hypochetical protein L163.04"
/product="hypochetical protein L163.04"
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SDITRAMLOOFMSAHITIVNGGRAADVEESVTAARVIPSANLFNUNTDANA
VLDAYDLLUDYGIAPESTLRILCKGSRMEYARHFTLVLKNANATSATQAHSPSPP
PRESPLASGGAGVAPVHTSAASTSTRASTASRRRDERSYFAQRIEELLE
ALKVLHRAEVGGTSLEGDTYINSALLRHYCRSTTPRHYLVLPPSSCAYRPGPVSDGV
RAASHVEGGGNSKGHPAANGFDLGPDPANEELLEGGGKSAVNEELEGLEGPGAPTRSRG
EPBAEKGRRRFRRPRQRDPYFRASSEEGTYILEVLKSYGSYPDNSVLQALSAQYEGQVPH
METVASAADAFFEGCMASHGTMSPVDCRFLHALGYYTINNRNVLEMFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYHVTFRADLSGTEKWFSYFAVIVGTKTGPLDLGIGLFAASLALSDKTVNPKVATKLT
AKRDSSEHVIEAIAELEKCGWDYHRILFCDALMLEPQERASAEKNESPAGANGAGSRD
HHHGRGANGSHAAGAVASSAAAAGEEHLGKESIYTSAGQGPSSYNNSHLLSARPSLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAYASPADLLPAPKAKASVLPDMFVHRESQQRTNGFYACVRCGTPVCEPSHQVIPASC
SLRGTAVFDALHMNGYBLRVCTPTVKGVAPPOSREQRESSPSPPAVKEJLGKVGGAABL
DVAGGLERFUHCRHCNGCLGWMRFGEITAPAAPATTLFCANSACLEYVPYRTRARL
DQSIWTDTGADPEASSGRGGGAASWFGRASAABHAQSRATIGSLFGPPHGAVAWGVE
GAIGVDYREEQGIISYAGDDTRLDASFDALLKDLDPCADLTPISSSVGSDG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADLVSRCSAPHFRTSAFLNVTADKDPKQEVTLSYHLMTDDAFGYGITGAKAVSRRDGH
AALDELAALFKKMFVEPPSTLNPKLADVFVRPARDLLMKYSSGAAAGSAENKVKKVKL
AVDEVKNMALDNVERVIQRGQRIDDIVQATDDLQFQABGFQRSSRDLRNQMWMSSMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDVPSRPSVAASSTAPOGRPKPRALALORSGGGALGSGRTORGE
SRVSGTAAIHGAPTRQPAHSERSGQRHTSSGTSLSIAANNAAAECSAPALPSTGCPAS
SAQQHGASVDLPYALHDMDEHFFTNRQNWKTEEELPGLVWSLLEGVTLEAPYTSHLWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="L163.06"
/note="L163.06, len = 256 aa, possibly synaptobrevin-like protein; carboxy terminus exhibits reasonable similarity to several, e.g. CAB71004 synaptobrevin-like protein (240 aa, Arabidopsis thaliana, EMBL: AL132957, CAB71004); Fasta scores: E():3.3e-09, 43.2% identity in 81 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MASNVNEESHALYGAVVVRLVDRVMLCKTPSAPMDGFT1PSTAW
                because we arrange for
    overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions. Cosmid Li63 is overlapped at the 5' end by L6294 (AL354533). THIS ANNOPATION IS PRELIMINRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6478. .7809)
/gene="L163.05"
/note="L163.05, len = 442 aa, unknown; uncertain translation start point, may use M120"
/codon_start=1
/label=L163.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="possible synaptobrevin-like protein"
/protein_id="CAB95269.1"
/db_xref="GI:8744981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein L163.05"
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/db_xref="GI:8744980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(<1. .2505)
/gene="L163.04"
/note="L163.04, len > 834 aa, unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMYVALRDLGVDKKTADWLRDKLKAARQEALASKRTR"
complement(6478, 7809)
/gene="L163.05"
                                                                                                                                                                                                                                                      /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="L163.06"
complement(10203. 10976)
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5664"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="cosmid L163"
complement(1. .2505)
/gene="L163.04"
                                                                                                                                                                                                                                                                                                /strain="Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=L163.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label-t163.04
                                                                                                                                                                                                                .27081
                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                see http://www.sanger.ac.uk/Projects/L_major/
CDS are numbered using the following system eg L163.01. L163
(COSmid name), 01 (first CDS)
To make the cosmid library Leishmania major Friedlin DNA was
partially digested with Sau3AI prior to cloning into BamHI site of
the cosmid shuttle vector CLHVG (Ryan et al. 1993 Gene
131:45-150). The sequence of the packaged vector was determined by
Peter Myler and Ken Stuart at Seattle Biomedical Research
Institute, and is available as accession number US9231.
The more significant matches with motifs in the PROSITE database
are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for
CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBHO 15A, (E-mail: barrell@sanger.ac.uk) and GATC GmbH, Fritz-Anold-Str 23, D-78467 Konstanz, Germany see http://www.ebi.ac.uk/parasites/leish.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation
                                                                                                                                                                     INV 23-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Details of leishmania sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the Log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the FramePlot program of Bibb et al., Gene 30:157-166(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pp. (2) codon preference based on the codon usage table for Leishmania at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-JUN-2000) European Leishmania major Friedlin genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: We may not have predicted the correct initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane domains were predicted as implemented at the TMHMM Server: http://www.cbs.dtu.dk/services/TMHMM-1.0/IMPGRTANT: This sequence Max NOT be the entire insert of the sequenced clone. If may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
Smith, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 27081)
Hilbert, H., Wedler, H., Wedler, E., Duesterhoeft, A., Ivens, A.C.,
Ouall, M., Rajandream, M.A. and Barrell, B.G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                  chromosome assembly protein; synaptobrevin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sult. U.S. A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                                     LMFL163 27081 bp DNA linear
Leishmania major Friedlin chromosome 21 cosmid L163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene prediction is done using:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.kazusa.or.jp/codon/
762 GGGCTTCTTCCAACCATCTCAGCA 785
                                                                                                                                                                                                                                                                                        GI:8744978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania.
1 (bases 1 to 27081)
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63

us-10-048-196-2.rge

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                           5967 GCTGTCATCAGCAGGCGCGCGCTCTCCTTCTTCCGTCGTTGTTGGGTGCGTCGCTG 5908
                                                                                                                                            6027 ACCGCTGTCGCCTACCCAGCTACACACGTGTACGCCTCTGTGGCTCAGTGTTGCGTGC 5968
                                                                                                                                                                                                                                                                                                                                                                                   100 nProAsnAlaArgThrGluValAlaGlnLysIle-----ValArgHisSerLeuLysPr 118
                                                                                                                                                                                                                                                                                                                   25 GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
                                                                                                                                                                                        pLysAlaProGlu------AlaValSerLeuThrGluLeuThrThrAlaAlaIleAs
                                                 6078 GAG------CGGCATTCTTTATCATTACTTTCGCGTTCGCTTTTTCTGCACCGCATC
                                                                                             45 LysGlnThrCysGlnThrGlnLeu---ThrGlyHisGlnTyrTrpLysIleAlaAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CF
***, 59 unordered pieces.
AC127124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC127124.2 GI:21903541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5791 TTGTCTC 5785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 oCysMet 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC127124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
AC127124/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                TSANAPASASSTGARASAASSPRDLESNAAGLSSKILNGSGSGGPSLDELRKVIL
TSANAPASASSTGARASAASSPRDLESNAAGLSSKILNGSGSGGPSLDELRKVIL
EVALLTSERNELRESKIVYTYVALOGSTLEGLØREHKDLATREASLLRKVEG
EVALLTSERNELREDSKILOFYSOLOTSSVINGLKAVEG
HEREDALRSLORKLDENSRREDPLLOFSSACSNVSRLCTGAKGEDVGSTDAAATEA
GEATEKAFAELQTKYHKRQQAAWEAAHDHAAAAAAYVVVRRYVMSNVPHSNYDAV
TFTGDAAALSTYFSSVGFEVENIAGERGRAHYTAASDALPFSSAPGFFGYARASLAR
TRAARAESSDAGAYTPAAFTYSAHPFVSAALLVRNAKCSVAYETARASGPGGGTNV
TETQYAKLTTDGYPATAFADDSRSALSNREAALDKLOQORRLOFNTLAKGENTV
VQAQLVAKMOHQGGRALEKDYHVLVQEBATAKLVAAGDVALVEMLQOLGVLAAAA"
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SIRGDGCYTENPAELSPLGKLPGTDETTGASIIVDVNPFISSALEAGDLLLTTVYTMQ
SFLTNQTNCWRLMAEAVWCMDGDDVGLDPRYMGSGAPGLAAWTESRDDPTVYPKSLME
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STSGGELPPPNIHHTDTIRNAVSGTSVMATVRQVFGGAVQATTLQTLHLGAPGESFGF
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                                                                                                                   /note="L163.07, len = 678 aa, unknown; uncertain
translation start point may use M113 (double methionine)"
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/db_xref="G1:8744983"
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/protein_id="CAB95272.1"
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/gene="L163.08"
/note="L163.08, len = 357 aa, unknown"
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/note="L163.09, len = 160 aa, unknown"
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complement(23013. .>27080)
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24 184024 bp DNA linear HTG 23-JUL-2002 norvegicus clone CH230-173B13, *** SEQUENCING IN PROGRESS

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NOTE: This is a "working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                          Vorley, K.C. Direct Submission Submitted (23-JUL-2002) Human Genome Sequencing Center, Department Submitted (23-JUL-2002) Human Genetics, Baylor College of Medicine, One Pavlor Plaza, Houston, TX 77030, USA
                                                                                           Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184024)
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y., Zhou,J., Zou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                    Daylor Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced g1:21744043.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                         Center project name: GLRJ
Center clone name: CH330-173B13
Center clone name: CH330-173B13
Center clone name: CH330-173B13
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 139590 bases at least Q40
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1 (bases 1 to 5857)
Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Bara,S.C.,
Fannon,M. and Dougherty,B.A.
                                                                                                                                                                                                                              57087 TAGCTITCAACTITCCTGTGCTTCTGTTTGTCTTGGGGATAAGGGACGAGTCTGCGAAAC
                                                                                                                                                                                                                                                                                     57267 ATTTTGGCCATATTTGGATCCACAAGGTGGGGTATCCAATACTCAGCCTCTTTTTCT
                                                                                                                                                                                                                                                                                                             33 AlaAsnLeuThrThrSerLeuIle-----LysHisAlaValLysGlnThrCysGln---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDV03/UB 5857 bp DNA linear PAT Polynucleotide of Streptococcus pneumoniae and sequence. BD003708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide of Streptococcus pneumoniae and sequence Patent: JP 2001501833-A 28 13-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 uLysProCysMetLeuGluThrValAsnAlaPheIleValProThrThr 133
            length
bp in length
                     contig of 4873 bp in length
gap of unknown length
contig of 6051 bp in length
gap of unknown length
contig of 4017, bp in length
 in length
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16
58
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Mismatches:
of 3654
unknown
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Matches:
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PN J 2001501833-A/28
PD 13-FEB-2001
PF 30-OCT-1996 US 60/OP
PI CHARLES A KUNSCH, GIL H
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JP 2001501833-A/28.
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Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Pettelin, H., Nelson, K.E., Paulsen, I.T., Haft, D.H., Dodson, R.J., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Undyam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Raduns, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T., Whitekey, E.K., Holt, I.E., Loftus, B.J., Yang, F., Smith, H.O., Venter, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.
                                                                                 C12N5/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00, PC
MICHAEL FANNON, BRIAN A DOUGHERTY
C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
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5016 AATGAAAATGATAACCTTACGACCAAATTAAAATTCATAGATGCCATGGTTACCGAG 4957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4896 CTAAAAGTTGCAGCGGTTAAAAAGACATTGAGGATAAAAGCAAGATGAGATGATGGATAAA 4837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 ---AlaValLysGlnThrCysGln------ThrGlnLeuThrGlyHisGlnTyr
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Streptococcus pneumoniae TIGR4
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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228
338
15

    .5857
    /organism='Unidentified'

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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1173 c 814 g 2070
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/organism="unidentified"
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Streptococcus pneumoniae TIGR4
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                                                                                                                                        Strandedness: Double;
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AE007414.1 GI:14972604
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88.50
48.54%
27.18%
13.09%
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ELSRLLWIELPELNESHKIEAVSKSTTGMFFAPGIFEMDAMRKAFFKROAKHFFENEA
EQOAYIEHAEKEYLEATVTLKDILFNSKNGTQKANKSCLIEKFEEAMO"
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DDLLNMKRAETGKALSPLQIQELQYMLEDFSPELIHEALKEAVSQGKANFAYIKVILN
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                                                                                                                                                                                                                                          4230. 4496
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4230. 4496
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/ 1980 - "SP1134"
/gene="SP1134"
/note="identified by Glimmer2; putative"
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/gene="SP1135"
/gene="SP1135"
/note="identified by Glimmer2; putative"
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/db_xref="GI:14972613"
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4230. .4496
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4507. 4650
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/transl_table=11
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/gene="SP1136"
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/gene="SP1133"
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S Tettelin, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D.,
Peterson, S., Heidelberg, J., DeBoy, R.T., Haft., D.H., Dodson, R.J.,
Durkin, A.S., Gwinn, M., Colonay, J.F., Nelson, W.C., Peterson, J.D.,
Umayam, L.A., White, O., Lewis, M.R., Radune, D., Holtzapple, E.,
Khouri, H., Wolf, A.W., Utterback, T.R., Hansen, C.L., McDonald, L.A.,
Feldblum, T.V., Angluoli, S., Gesuwan, P., Hickey, E.K., Holt, I.E.,
Loftus, B.J., Ujwal, M.L., Yang, F., Smith, H.O., Venter, J.C.,
Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.
Direct Submission
Losulted (29-JW-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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VEETLAAIEAAGYVPGKDVFTGFDGASSEYVDKERKVDYTKFEGEGAAVRTSAEQID
YLEELVNKY PIITIEDGAMDENDWDGWRALTERLGKKVQLVGDFFVTNTDYLARGIOE
GAANSILIKTWONGTLTETFEALEMAKEAGYTAVVSRRSGETEDSTIADIAVATNAĞQ
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PVFGDYKLSKLTTPILQQOVNKWADKANKGEKGAFANYSLLHNMNKRILKYGVAIQVI
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CRESESEAAGYRDIPLESOYISINKTLNRYQBUSRKSASGYRDIPLDKATLLLLK
QYKNRQOIGSNKLASESTVVESYTEKYAAQNLKRELNKHFDAAGYRNVSFHERHT
HTTMMLYAQVSPKDVQYRLGHSNLMITENTYWHTNQENAKKAVSNYETAINLL"
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KACQLAQNTISKIDYOISDETIKKFIDLAIDSORDLGGNLLKNNLSNEDYSLEGGTRN
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DYIAPSEIVSFSTYVRQRSKVIPKILEHILKSSFLLENIDVSGYTVNILEDQLYRHRI
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/db_xref="GI:14972606"
  Complete genome sequence of a virulent isolate of Streptococcus

    .11849
/organism="Streptococcus pneumoniae TIGR4"
/strain="TIGR4"

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                                         Science 293 (5529), 498-506 (2001) 21357209
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complement(1571. .2734)
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113. .1417
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3777. .4130
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                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Jul 9, 2002 this sequence version replaced gi:20467446.
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                                                                 AC111203.5 GI:21716965
HTG; HTGS_PHASE1.
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       unordered pieces.
                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                             Norway rat.
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                                                                                                                                                                                                                                                                                   Rattus.
                                                                                                                                                                          . ORGANISM
                                ACCESSION
VERSION
KEYWORDS
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/protein_id="COTE:14972614"
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/translation="MSCIQSEGG"
/tra
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Rattus norvegicus clone CH230-7H1, *** SEQUENCING IN PROGRESS ***,
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|8262 AATGAAAATGATAACCTTACGTCCAAGCAAATTAAAATTCATAGATGCCATGCTTACCGAG 8321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MVSLPHLVYMVVESMAITSQRAISHPMKSVYFCLGL" 7556. .8206
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NWKQDNLLTVELVRNSRAAREAKKQQTNQLEPTSYEDWIPTQEKPF"
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/gene="SP1138"
/note="identified by Glimmer2; putative"
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/note="identified by Glimmer2; putative"
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                                                                                                                423. .7307
gene="SP1137"
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                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid; Sequencing vector: plasmid; Assemblery: Dye-terminator Big Dye: 100% of re-Assembly program: Phrap; version 0.990329 Consensus quality: 178995 bases at least 040 Consensus quality: 182795 bases at least 030 Consensus quality: 188082 bases at least 020
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Db 153702 -	ACTGGCCACAGAACCTGGAAGCATTGCAAGCATTTCC 153743	Db 139
Oy 67 St	erGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla 82 	0y 10
Db 153744 T	TCCCACCTTTCTGTGTGAGAACCTGCCAGGAACAAGTTGTCTATCCTACGTTGCATGTCC 153803	Db 144
Oy 83 As Db 153804 C	AspLysAla	0y 12 Db 149
Oy 96 TI Db 153864 Av	ThralaalaileasnProasnalaargThrGluValalaGlnLysIleValargHisSer 115 ::: : aagGCCTTGCTAACCCCTCCTGCTA-CCCCATGTCCCCAAGTCTAGCAGTAGATGGAGC 153922	RESULT ? TAGLIAA LOCUS
Oy 116 Lo Db 153923 C	LeuLysProCys 119 	DEFINITA ACCESSIC VERSION KEYWORDS
RESULT 23 103335 LOCUS	, ,	SOURCE ORGANI
DEFINITION ACCESSION VERSION KEYWORDS	Sequence 2 Irom Patent US 4826/65. 103335.1 GI:270041	REFERENC AUTHOI TITLE
SOURCE ORGANISM	Unknown. Unknown. Unknown.	JOURN
REFERENCE AUTHORS TITLE	Victorial to 2000) Greene, F.C., Stiles, J.I., Neill, J.D., Anderson, O.D. and Litts, J.C. Yeast strains genetically engineered to produce wheat gluten	PUBMI PUBMI FEATURES SOU
JOURNAL	-MAY-1989; ica as repre	re
FEATURES	<pre>Lne; washington, UC Location/Qualifiers 1. 2000</pre>	rep
BASE COUNT	/Organism="unknown" 686 a 481 c 352 g 480 t 1 others	rei
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0у 22 -	SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu 39	
Db 1173 A0	ACAACAACAACAACAACAAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 1232	
Qy 40 I	IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys 59	
Db 1233		
Oy 60 I.	IleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer 74	rep
Db 1275 AC	ATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT 1334	rep
Oy 75		rep
Db 1335 A	ATGGCAGATCCCTGAGCAGTCGCAGGCCATCCTCAAAGTTGTTCATGCTAT 1391	mis
Qy 83 As	AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102 ::: ::	mis

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/protein_id="aa25593.1"
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/d
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Wheat gene for storage protein gliadin (A-gliadin subgroup).
X01130
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Anderson,O.D., Litts,J.C., Gautier,M.F. and Greene,F.C.

Nucleic acid sequence and chromosome assignment of a wheat storage protein gene

Nucleic Acids Res. 12 (21), 8129-8144 (1984)

85062803
                                                                                                                        140 CTCCTTCCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCCG 1490
----TATTCTGCATCAACAACAACAACAACAACAACCATCGAGCCAGGT 1439
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/note="imp. inverted repeat D'"
1640...1650
/note="imp. direct repeat E"
1651...1661
/note="imp. direct repeat E"
1710...1715
/note="pot. polyadenylation signal"
/note="pot. polyadenylation signal"
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/note="storage protein (aa 1-286)"
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gliadin; inverted repeat; storage protein.
Triticum aestivum.
Triticum aestivum
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/note="pot. TATA-box"
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/note="imp. inverted repeat D"
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/note="imp. inverted repeat B"
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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/note="inverted repeat A"
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/note="pot. TATA-box"
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Direct Submission
Submitted (02-AUG-2002) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Aug 11, 2002 this sequence version replaced gi:21953218.
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.
                                                                                                                                                                                                                                                                                                                       Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41412 GATAACAGAAATTAAAGCATGTGCAGCGCTTTCTTCCGCATCACATGGTCTTATAGCTGA 41353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 SerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 31145: contig of 31145 bp in length 31146 31245; gap of 100 bp 77566 77665; contig of 46320 bp in length 77566 7865; gap of 100 bp 77666 85328: contig of 7663 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31145 bp contig from 1 to 31145
46220 bp contig from 31246 to 77565
7663 bp contig from 77666 to 85328
14726 bp contig from 87599 to 100154
57108 bp contig from 100255 to 157362,

* NOTE: This is a 'working draft' sequence. It currently
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/sub_species="japonica"
/db_xref="taxon:4530"
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                      Oryza sativa chromosome 12
Unpublished
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                                                                                   (bases 1 to 157362)
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Arentz-Hansen, E. H.
Direct Submission
Submitted (05-MAR-1999) Arentz-Hansen E. H., Institute of
Immunology, University of Oslo, Rikshospitalet, N-0027 Oslo, NORWAY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooddeae; Triticeae; Triticum.

1 (bases 1 to 810)
                                                                                                                                             41298 AGTTGCCTCAGCAAACCCAACATAGCCATCTGCTACAGGACGGCAACTGTATCGTGCCTC 41239
                                                      41352 AATACCCTGTGCACGAACAACAAAGGCTCTCCA-----ACTCCTCTTGCACCATAAAC 41299
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                                                                                                             rThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSe 115
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alpha-gliadin storage protein,
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  uThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuTh
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Indels:
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Matches:
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257 c 125 g 15
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Triticum aestivum.
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Best Local Similarity:
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AUTHORS
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JOURNAL
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FQQPLQOSYPQLLGGECCQHLWQIPEGSSQVQPQQLPGFEIRNLALQTLPAMCNVXIPPY
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Triticum aestivum subsp. spelta.
Triticum aestivum subsp. spelta
Triticum aestivum subsp. spelta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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Kasarda, D.D. and D'Ovidio, R.

Beduced amino acid sequence of an alpha-gliadin gene from Spelt
wheat (Spelta) includes sequences active in celiac disease

Cereal Chem. 76, 548-551 (1999)
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Submitted (23-NOV-1998) D'Ovidio R., Agrobiologia e Agrochimica,
Universita della Tuscia, Via San Camillo de Lellis I-1100 ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                             482
                                                    321 ACAACAACAACAACAACAACAAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 380
                                                                                                                                                                       ------CATGGATGTTGTATTGCAGCAACACACATAGCGCATGGAAG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                    S88 CTCCTTCCAACAGCCTCTGCAACAATA----TCCATTAGGCCAGGGCTCCTCCG
-----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
                                                                                                               40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                        -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                             183 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn
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218. .>1081
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218. .1081
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639 GCCATCTCAGCA 650
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218277 gene="alpha-gliadin" gene="alpha gliadin" gene="alpha gliadin" forduct="alpha gliadin" 7981081 7981081 337 c 161 g 221 t 8.25 Length: 8.25 Length: 87.00 Matches: 36.99% Conservative:	ນ ລັບັຄັ∵≷ເ		Db 817 TATTATTCTGCATCAACAAAACAACAACAACAACAACAACAACAACAACA		AUTHORS Sumner-Smith,M., Rafalski,J.A., Suglyama,T., Stoll,M. and Soll,D. TITLE Conservation and variability of wheat alpha/beta-gliadin genes JOURNAL Nucleic Acids Res. 13 (11), 3905-3916 (1985) MEDLINE 85242077 PUBMED 3839304 FEATURES Location/Qualifiers Source 1. 1672

0y 60 11e	Oy 103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122 ::::	AL urce S	Alignment Scores: Pred. No.: Score: Score:
ION Wheat mRNA for gliadin. X00627 K03076 X00627.1 G1:21752 gliadin; signal peptide. Triticum aestivum. Triticum aestivum. Triticum aestivum. Spermatophyta: Magnoliophy Pooideae; Triticeae; Triti	TOO A T T T T T T T T T T T T T T T T T	sig_peptide 596. 655 mat_peptide 656. 1453 mat_peptide 656. 1453 /product="gliadin" /note="aa 1-266" polyA_signal 1534. 1539 /note="put. polyA signal" /note="put. polyA signal" polyA_site 1620 polyA_site 1620 /note="pot. polyadenylation site"	Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Developmentally regulated plant genes: the nucleotide sequence of a wheat gliadin genomic clone EMBO J. 3 (6), 1409-1415 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 27-APR-1993 clone pW8233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gliadins, the major wheat seed storage proteins, are encoded by a multigene family and are highly conserved. In the sequence presented here a TATA box is located at positions 492-499 and potential poly-A signals at 1534-1539 and 1591-1596. Four P-boxes (containing many proline codons) are found at 758-793, 794-829, 830-868, and 869-904. The P-box presumably arose in the ancestral alpha/beta-qliadin gene and was multiplied prior to the extensive multiplication of the whole gene. Every P-box is slightly different from every other. Two polyglutemine stretches reside at 941-994 and 1202-1224. In wheat DNA 'cg' and 'cng' sequences are over 80% methylated to m5c. An alternating purine pyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summer-Smith, M., Rafalski, J.A., Sugiyama, T., Stoll, M. and Soell, D. Conservation and variability of wheat alpha/beta-gliadin genes Nucleic Acids Res. 11, 3905-3916 (1983)
2 (bases 1 to 3022)
Rafalski, J.A., Scheets, K., Metzler, M., Peterson, D.M., Hedgcoth, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                      1240 CTCCTTCCAACAGCCTCTGCAACAATA-----TCCATTAGGCCAGGGCTCCTTCCG 1290
                                             973 ACAACAACAACAACAACAACAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 1032
                                                                                                                                           1033 -------CATGGATGTTGTATTGCAGCAACATAGCGCATGGAAG 1074
                                                                                                                                                                                                                                         1075 ATCACAAGTTTTGCAACAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
                                                                                                59
                                                                                                                                                                                                 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wheat (T.aestivum cv. Yamhill) endosperm, cDNA to mRNA, clone pW8233 [2],[3].
----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu 39
                                                                                             40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                       83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn
                                                                                                                                                                                                                                                                                                                                     1135 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT---
                                                                                                                                                                                           60 Ile------AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                         -----GluThrAlaCysGlyCysValAla
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Sequence in computer-readable form provided by D.Soell,
04-JUL-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHTGLIABE 3022 bp mRNA linear Wheat (T.aestlvum) alpha/beta gliadin class I gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 3022)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soell,D.
Unpublished (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ThrValAsnAla 126
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K03076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (sites)
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL
COMMENT
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AUTHORS
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PUBMED
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KEYWORDS
SOURCE
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PLN 17-APR-2002
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Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0446B05.
stretche with 2-forming potential lies between nucleotides 2258 2281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    973 ACAACAACAACAACAACAACAATCCTTCAACAAATTTTGCAACAACAACTGATTCCATG 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1135 ATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCATGCTAT--- 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 -----SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TATTCTGCATCAACAAAAACAACAACAACAACAACCATCGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1075 ATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCAACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 -----GluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                             /note="alpha/beta-gliadin signal peptide"
656. 1453
/realpha/beta-gliadin"
/realpha/beta-gliadin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3022
36
17
53
38
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                                                                                                                                                                         /note="alpha/beta-gliadin precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
                                                                                     aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                             529, .1626
/product="gliadin mRNA"
596. .1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x WHTGLIABE (1-3022)
                                                                                              /db_xref="taxon:4565"
529, .1626
                                                                                                                                                                                                                                                                                                                                                                                                                   1021 a 741 c 521 g
1 bp upstream of HindIII site.
                                                                   1. .3022
/organism="Triticum
                                                 Location/Qualifiers
                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 655
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                  1021 a
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                                                                      source
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AP003251/c
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Q
                                                                                                                    mRNA
                                                  FEATURES
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oin(22593. 23216,24099. 25639,26226. 26367,26499. 26606,
26691. 26903,26990. 27100,27933. 28127,28751. 28925,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BabB9556.1"
/db_xref="G1:20160610"
/translation="MGEEKCIAMGNNAGQSQARHTRLPDDVVETSKDDIIVQDYTTTGS
LVDDXQSHCRRORVPPMPYSSPGLHDALFGLDTIILDDEDEHHSRIMRSNSNMRHNDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDILAAISNMMMSKDGTLGDSNSISQSKFQSEISDHQNISLDPKALQVNKNQHSLMLE
ADTDYLGIPPISQPSNPSFSDINKNVSGLANIRNSTNTRIDGHAEMQRSSTLSTRSYQ
KSPTSSNASPGGSPAQHQNIDNINSAFLNYGLGGYPLSPGLPSMMMNCMGSGNMPPLF
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TFYGQVVPLSTHPYGCRVIQRVLEHCTDPKTQEIVMDEILQSVCMLAQDQYGNYVVQH
VLEHGKPHERSVIIEKLAGQIIQMSQQKFASNVVEKCLTFGGPAEREVLINEMLGTTD
                                                                                                                                                                                                                                                                                                                                           ALATEVFTVGGPPLRAAFGCMATÄPDTSPDGVATAGLLGMNRGALSFVSQASTRRFS
YCISORDDAGVYLLGHBOLPFLLATPLYOPAMPLPYFDRAYNXVOLLGINVGGKPL
PTPASVLADPHTGGGTWUNSGTOFFFLLGDAYSALKAEFSRGTKPRLPALNDPNFAF
OEAFDTCFRVPQGRAPPARLPAVTLLFNGAQMTVAGDRLLYKVPGGRRRGGDGVWCLTF
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VFSQNVGFDQEEAARNDVGGAAEWVDGGGDGL1GLSLGRQRSFAD1LQDN1GRRTPAS
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FASVLGSSISRNATPDSHYVPRVPSPGLPPVGVRINSNEKKLNCSSSFNTASSKAVEP
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TTSNHGYYGNLAFGMGMAYPGSPLGSPVASPSGPGSPLRLSERNMRFPSNLRNLGGWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MATFSTAGGIGMDASPIWCFMCSRLHRPDGLSTCPTRAPRAALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIVEVMDAGEFLQACALRRAPVAAAVSSTRQQLPTVTVRDAGRTCAVCLDDLEPGGSA
VVTPCDHAYHPQCIAPWLEAHDTCPLCRRESGLQVVEVEVQVDGMVLSSPDGLVLCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMPGGRSEYRLGRRVAGRIFAVRVVDGTGKLVRGGVLRRLGSACHRFAAAAGNLLSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDPSGYMNDNFPSSLLDEFKSNKARSFELAEIASHVVEFSADQYGSRFIQQKLETATV
                                                                                                                                                                                                                                           /translation="MPPPPALPVCLLLLLLLAVPRPAAAAAAAAATRPLLFELRAR
QVPAGALPRPASKLRFHHNVSLTVSLAVGTPPQNVTWVLDTGSELSWLLCAPGGGGGG
                                                                                                                                                                                                                                                                                                                  GGRSALSFRPRASLTFASVPCDSAQCRSRDLPSPPACDGASKQCRVSLSYADGSSSDG
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FRSGSAPPTIEGSLNAISGLLRGGGEAAVTVAAIPDAETLNGHGGLLSEDELRADPAY
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26691. .26903.26990. .27100,27933. .28127,28751. .28925,
29066. .29103)
/gene="PQ446B05.5"
                                   /note="contains EST AU176487(E21047)
similar to Arabidopsis thaliana chromosome 5, At5g02190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNADMVPITAYVIGHHQMNVWVEYDLERGRVGLAPIRCDVASERLGLML"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(13981. .14067,14601. .14684,14736. .14909)
/gene="P0446B05.3"
join(13981. .14067,14601. .14684,14736. .14909)
/gene="P0446B05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein"
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complement(17162. .17869)
/gene="P0446B05.4"
/note="hunder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB89557.1"
/db_xref="G1:20160611"
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/db_xref="GI:20160612"
                                                                                                                                                                          /protein_id="BAB89555.1"
/db_xref="GI:20160609"
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/qene="P0446B05.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission

Direct Submission

Submitted (19-FED-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, 7el:81-298-38-7441, Fax:81-298-38-746)

On Apr 16, 2002 this sequence version replaced gi:17933036.

Genes were predicted from the integrated results of the following: CENSCANI.0, BLASTNX.0, BLASTNX.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RRP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0, ESTS represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone in.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein name to indicate the homology (covering almost the entire length of partial sequence) is classified as an is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to 77 of the PAC clone. This sequence of P04466605 clone has an overlap with P046608 clone. Thurst.applia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DDBJ:AP003240) clone at the position 1 to 17,096 of 5' end and with P0005410 (DDBJ:AP004127) at the position 98,039 to 149,145 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at
                                                                                                                                       clone:P0446B05.

Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae;
                                                                                                       sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains ESTs D23149(C2313),C26277(C12019) similar to Arabidopsis thaliana chromosome 3,At3g09320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(1108. .1218,2391. .2486,2568. .2681,
2756. .2833,2914. .3015,4386. .4661))
/gene="P0446B05.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(1108 .1218,2391 .2486,2568 .2681,
2756 .2833,2914 .3015,4386 .4661))
/gene="P0446B05.1"
                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

    1. 149145
    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11360. .12688)
/gene="P0446B05.2"
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complement(11360. .12688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB89554.1"
/db_xref="GI:20160608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in Database (2001)
                                                                                                                                                                                                                                                                           Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="P0446B05"
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                                       GI:20160607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 149145)
Sasaki,T., Matsumoto,T
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                      clone: P0446B05
                                       AP003251.3
                                                                                                          Oryza
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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                                                                                                       SOURCE
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.26606,

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Augestsour, volumission
Submitted (14-MAR-1996) Olin D. Anderson, Western Regional Research
Center, Agricultural Research Service, USDA, 800 Buchanan Street,
Albany, CA 94710, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                       TAU51306 3034 bp DNA linear PLN 10-APR-1996
Triticum aestivum alpha-giladin storage protein gene, complete cds.
U51306
                                                                                                                                                                                                                                                                                                                                                                           wheat strain=Cheyenne.
Triticum aestivum
Eukaryota: Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 3034)
                                                                                                                     AGTIGCTCAGCAAACCCAACATAGCCATCTGCTACAGGACGGAACTGTACGTGCTC 67399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 GTATTCGCAACCACAACAACAATTTCACAGCAGCAGCAGCAGCAGCAACAACAACA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 ThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGln 56
                     uThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuTh
                                                        AATACCCTGTGCACGAACAACAAAGGCTCTCCA-----ACTCCTCTTGCACCATAAAC
                                                                                             rThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr
                                                                                                                                                                                                           67356
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36
17
53
41
6
                                                                                                                                                                       rLeuLysProCysMetLeuGluThrValAsnAlaPheIleVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wheat seed storage protein"
                                                                                                                                                                                                           ATTTGCGCCTATGCCTCTCAAAACCTCAGATAGCAACGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Cheyenne"
/db_xref="taxon:4565"
/clone="CNN52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                         U51306.1 GI:1256790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.7
86.50
36.05%
24.49%
12.80%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
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                                                                                                                                                                                                                                                                                                  DEFINITION
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                   7.5
                                                        67512
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                                                                                                                                67458
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                                                                                                                                                                                                                                              RESULT 33
TAU51306
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KEYWORDS
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50835. .51009,51135. .51314)
/gene="P0446B05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(49471. .49582,49670. .49766,50360...50423,50591. .50619,
50835. ...51009,51135. .51314)
                                                                                                                                                DEDDDEDEEGEGEGGODDAPAAAAGGGGGCGKCKKARMWTPELHHRFVEAVAHLGEK
GAVPKAIVRLMNVDGLTRENVASHLQKYRLYLKRTRVAATPPPSPPPPPPPPPPAA
MYVPCFAAKPPLDAANRSDSPPSRTSDATTKQ"
                                                                                                                                                                                                                                                                                                                                                     /translation-*MMMPVDLRLPSGPQAALGILAFEAAAANSKLLSLHRSLSEGEVS
REREDTMRSPGVAYLNSTDQAFLLRLACAELVVSLDAAAAVARLGFRCGIDEGGVA
SLKAGAPDDARLDPLVAKGLRTVAKKKRRRLVSSTRATLCSEMEALDELESERRLAFRGW
NRLSGPIPMOPVAPSAAGDSFGADSLOGDLKAQRIKVRRLKEESLWNOSYBRAVGLMA
RAACAVFSRICTIFGAFVPGLPPPLPSAATDSVQTRLSKLLNPRAVRAKASSGPITRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:20160615"
/translation="MITDLEATFWTCTGVKOILQDSCGGRRILELGDVAKKGRSWGVG
DVAVAAAGRWRMLORFWTCTROKGTIGPAKWDEKWREREEFETARRKIALCATLF
RSAVWPYPLLIMRRRWTVYARGGKTGRRRKYECSGAREQDWGVHDRFSIGSDLLLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAB89562.1"
/db_xref="GI:20160616"
/translation="MTNICAYRARTPNNNSDGPSSKRSRDQPRDRCTHSFSPSGDTQK
                                                                                                                              /translation="MTPVSHQLVPPALAAAFGIDLAAVGVLLPSPSVDSPVSHLFFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGPSRVHPPVISSSCPIIGLRPSGQKAAIDWRKLLDAPASTVGGAGLDQQYANVIVSA
EQLLQMEAEGRQEEANAERAEMYEMLPAKLRAAVRSKLRDWWRDPGPLDAGLAQGWKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVDRIMAWLGPMARDTVQWQAERNMDRTRRFDGGARVYALQTLRWADKEKAEAALVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67572 GATAACAGAAATTAAAGCATGCGGCGTTTCTTCGCGCATCGCATGGTCTTATAGCTGA 67513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67633
                                                                                                                                                                                                                                                                                                /product-"putative Avrg/Cf-9 rapidly elicited protein"
/protein_id-"BAB89560.1"
/db_xref-"GI:20160614"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pLysIle-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(43392. .43820,43852. .43917))
/gene="P0446805.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(43392, .43820,43852, .43917))
/gene="p0446B05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149145
35
19
54
7
                                     /note="contains EST AU082886(C53868)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"hypothetical protein"
                                                                                                                                                                                                       complement(40152. .41567)
/gene="P0446B05.7"
complement(40152. .41567)
/gene="P0446B05.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                         /protein_id="BAB89559.1"
/db_xref="GI:20160613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id-"BAB89561.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                     1195 TGCTAT------TATTCTGCATCAACAACAACAACAACAACAACCATC 1239
                                                                                                                                                                                                                                                                                                                                                                                                         1240 GAGCCAGGTCTCCTTCCAACAGCTCTGCAACAATA-----TCCATTAGGCCAGGG 1290
-----CATGGATGTTGTATTGCAGCAACACACATAGT 1074
                                                                                      1135 TCAGCACCTATGGCAGATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAATGTTGTTCA 1194
                                                                                                                                                                                                                                                                                                                                                                     100 AsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys 119
                                                                                                                                                                                                                                                                         66
                                                  57 TyrTrpLysIle-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIle 73
                                                                                                                                                               -- GluThrAlaCysGly 79
                                                                                                                                                                                                                                                                80 CysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlalle
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Rattus norvegicus
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1033 GATTCCATG-----
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KEYWORDS
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA on Jul 18, 2002 this sequence version replaced gi:20976348.

Center: Baylor College of Medicine
                                                                                                                                        Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 133255)
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 83898 bases at least Q40 Consensus quality: 88833 bases at least Q30 Consensus quality: 92150 bases at least Q20
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1381: gap of unknown length
2440: contig of 1059 bp in length
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Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GXFA
Center clone name: CH230-521B13
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Rattus norvegicus clone CH230-262L23, *** SEQUENCING IN PROGRESS ***, 63 unordered pleces.
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alibabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Breva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chen, C., Chowald, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Daland, M.L., Daland, M.L., Daland, M.L., Daland, C.D., Cox, C., Elbaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Ealls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Gabisl, A., Gao, J., Garda, A., Garner, T., Garza, N., Gill, R., Gabisl, A., Garcial, A., Garner, T., Garza, N., Gill, R., Garrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
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Mammalia; Eutheria; Rodentla; Sclurognathi; Muridae; Murinae;
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Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hornandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia Y., Ohnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia Y., Ohnson, R., Jolivet, S., Joudah, S., Karlsshi, A., Landry, N., Leal, B., Korvah, J., Kovar, C., Kartosio, J., Kiracehi, A., Landry, N., Leal, B., Lu, M., Loulseged, H., Lozado, R.J., Lit, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, D., Newtson, M., Nguyen, A., Martinez, E., McGod, M. P., Newtson, M., Nguyen, N., Okwoon, G., Oragunye, N., Noideo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, D., Le., Quiles, M., Okwoon, G., Oragunye, M., Oviedo, R., Pace, A., Payton, B., Stonaike, T., Stonaike, T., Stonaike, T., Stonaike, T., Stonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Wang, Q., Wang, S., Warten, R., Washington, C., Watlington, S., Wang, S., Walt, W.Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wole, S., Warlen, R., Washington, C., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Mare, R., Washington, C., Wang, S., Chandel, R., Stonaike, R., Washington, C., Wallians, G., Walliams, G., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20330712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 185108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2: contig of 1022 bp in length-
2: gap of unknown length
7: contig of 1015 bp in length
7: gap of unknown length
8: contig of 1186 bp in length
1: gap of unknown length
1: contig of 1257 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .------ Project Information
Center project name: GVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 185108)
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TITLE JOURNAL REFERENCE AUTHORS

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COMMENT

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Arentz-Hansen, E.H.
Direct Submission
Submitted (05-MAR-1999) Arentz-Hansen E.H., Institute of
Immunology, University of Oslo, Rikshospitalet, N-0027 Oslo, NORWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OOQQOQOQILQQILQQQLIPCRDVVLQQHNIAHGSSQVLQESTYQLVQQLCCQQLMQI
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ------AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGlu 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 ASPProLysAspSerSerAlaAspLeuThrThrSerLeuIleLysHisAlaValLysGln 46
                                                                                             1 (bases 1 to 822)
Arentz-Hansen, B.H., McAdam, S.N., Molberg, O., Kristiansen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 ACAACAACAAATCCTACAACAAATTTTGCAACAACAACTGATTCC-----ATGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ThralaCysGlyCys-----ValAla
                                                                                                                                    Production of a panel of recombinant gliadins for the characterisation of T cell reactivity in coellac disease Unpublished
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 - 819
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261 c 130 g 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-048-196-2 (1-134) x TAE133604 (1-822)
   alpha-gliadin; storage protein.
Triticum aestivum.
Triticum aestivum
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/clone="alpha-7"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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36.81%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 bp mRNA linear PLN 06-MAR-2
Triticum aestivum mRNA for alpha-gliadin storage protein, clone
alpha-7.
AJ133604.1 GI:7209248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34283 ---GTCCCACACATCCATCAGGTGTTTGCTGTTTGGGTTTCTGAGATAGAGCCTAACAGG 34227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 SerGluSerLysAlaLys-----IleSerGluThrAlaCysGlyCysValAlaAsp
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25.19%
12.80%
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Best Local Similarity:
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VERSION
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1129 GCATAAGCCGCAATAGCCGCAGCGGGATGCTTTTGACTGGCCTTGCTTAAGTATTCCAGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 3823)

1 baser. F. W. Burland, V., Perna, N.T., Plunkett, G. and Welch, R. Sequences of E. coli 0157

Patent: US 6365723-A 132 02-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------MetLeuGluThrValAsn 125
                         600 CTCCTTCCAACAGCCTCAGCACAATA-----TCCATCAGGCCAGGGCTTTTTCCA 650
103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu 122
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                                                                                                                                      linear
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Conservative:
Mismatches:
                                                                                                                                    AR204236 3823 bp D1
Sequence 132 from patent US 6365723.
                                                                                                                                                                                                                                                                                                                                                                                              Length:
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                                                                                                                                                                                                                                                                                                                          /organism="unknown"
961 c 900 g
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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85.50
36.918
22.15%
12.65%
                                                  ThrValAsnAla 126
                                                                    |||:::::|||
| 651 ACCATTTCAGCA 662
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Best Local Similarity:
Query Match:
DB:
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AE005438/c
                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                         RESULT 37
                                                                                                                                                                                                                                             REFERENCE
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carriers: Molybdopterin"

Anote—"Residues 3 to 962 of 963 are 32.44 pct identical to residues 230 to 1209 of 1210 from Escherichia coli K-12 Strain MG1655: B2118"

/codon_start=1
/transl_table=11
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/product="putative regulator (fragment)"
/product="putative regulator (fragment)"
/product="putative regulator (fragment)"
/protein_id="AAG57176.1"
/db_xref="G1:12516331"
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VAAABKAKLKIAEKTKKGYVENASANVHIPPITKATPEVETSPESKNGRPWIADAV
IPVTDDINMFAFPHRSRPREINYLRKDGEIWKRIADNTRAYDPDNNYRSYPENWQQAF
AELQRALLDNQQTGSAQSDAALLMSFWNSYSADELVDDLVIRGGLESAVEIVLFALQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Residues 1 to 218 of 242 are 37.75 pct identical to residues 1 to 244 of 274 from Escherichia coli K-12 Strain MG1655: B2115"
AE005438 . . 11010 bp DNA linear BCT 21-MAR-2001 Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 57 of 290.
AE005438 AE005174
AE005438.1 GI:12516330
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//note="0-island #90; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
1019. .3910
                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Maybew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                    l (bases 1 to 11010)
Pernah NT., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Kilnk, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
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    11010
/organism="Escherichia coli 0157:H7 EDL933"

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Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /serotype="0157:H7"
/db_xref="taxon:155864"
/note="enterohemorrhagic"
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                                                                                                                                                               Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="EDL933
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/note="Z3284"
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/gene="molR_B"
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/note="Z3283"
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SOURCE
ORGANISM
                            DEFINITION
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AUTHORS
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MEDLINE
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/translation-"MDKELPWLADNAQLELKYKKGKTPLSHRRWPGEPVSVITGSLIQ
TLGDELLQQAGKENITWNYDKCSLEWQSAIQQAINLTGEHKPSIPALTMAALICIAQ
NDSQQLLDELVQQEGLEYATDVVISKQCIARRYESDSLVVTLQYQDEDYGYGYGSATY
NDFDLERRKHLSLAEESCWQRCADKITAALFOIPKIRRFIALILPERPETALICIAG
SSRSSLHSKEWLKVVATDNTAVKKLERYWGLDVFSDREASYMSQENRFGYAACASLL
REĞGLAAVPRLAMYAHKEDCGSLLVQINHPQYTRTLLGYADKNKPSLQRVAKYSKNEP
HATLAALAELALKEPPARGYPILEDKKLFQQOKARESYWRTLQTLMASQPQLAAE
VMSWLSTQARAVLKS LSALPKPYIDGTDNSNLPEILVSPPWRSKKWMPPRLDLARL
ELTPQYYWQFGERERLAATESARYFSTESLAQRMEQKSGRVVLQELGFGDDVWLFLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILPCKLDAARNSLIVOWHYYOGRVEEILNGWNSPEAQLAEQALRSGHIEALINIWEND
NYSRYRPEKSVWNLYLLAQLPREMALTFWLRINEKKHLFAGEDYFLSILGLDALPGLL
LAFSHRPKETFPLILNRGATELALPYARVWRRFAAOROLAROWILOWPEHTATALIPL
LAFSSHRPKETFPLILALLALLELYEHGHGELQTVANRWOGYTDWAPALFHLKKOGPWEIYPA
RIPKASDKSEAALLALLITTNNOPYTDDALEIIGEMLRFTQGGREYSGLEQLKTFCO
PQYLAAFAWDLFTAWQOAGAPAKDNWAFLALSLFGESTARDLTTQILAWPQGKSARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSGLNILTLMNNDMALIQLHHISQRAKSRPLRDNAAEFLQVVAENRGLSQEELADRLV
PTLGLDDPQALSFDFGPRQFTVRFDENLNPVIFDQQNVRQKSVPRLRADDDQLKAPEA
LARLKGLKKDATQVSKNLLPRLEAALRTTRRWSLADFHSLFVNHPFTRLVTQRLIWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="orf; Unknown function"
/note="Residues 1 to 105 of 105 are 99.04 pct identical to
residues 1 to 105 of 105 from GenPept 118 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAG57181.1"
/db_xref="G1:12316336"
/translation="MIVQFEVAIYDYEVPVPEDPFSFRLETHKCSELFTGSVYRLER
FRRSFFHQRDREDAPLINDALIYIRDECIDERKLRGESSPETVIAIFNRELQNIFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPANEPRRLLNAFRVAAEGGFCNAQDEPIDLPADALIGIAHPLEMTAEMRSEFAQLFA
DYEIMPPFRQLARRTVLLTPDESTSNSLTRWEGKSATVGQLMGMRYKGWESGYEDAFV
YDLGEYRLVLKFSPGFNHYNVDSKALMSFRSLRVYRDNKSVTFAELDVFNLSEALSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gil405847|gb|AAA60479.1| (U00007) yehk [Escherichia coli]"
                              /function="putative regulator; Not classified"
/note="Residues 1 to 1209 of 1209 are 94.04 pct identical
to residues 1 to 1210 of 1210 from Escherichia coli K-12
Strain MG1655: B2118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="O-island #91; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
2709 c 2653 g 2631 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrValThrAlaThrLeuMetThrAlaPhe---ThrLeuAlaSerCysAlaSerThrPro
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Conservative:
Mismatches:
                                                                                                                                                                                           /transl_table=11
/product="putative regulator"
/protein_id="AAG57180_1"
/db_xref="G1:12516335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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/transl_table=11
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10609. 10926
/gene="yehk"
/note="z3288"
10609. 10926
/gene="yehk"
                                                                                                                                                                /codon_start=1
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                                                                                       /translation="MTWLRLVITDDTALSTVEKYDFPPLYRDFRNFRAYLAMLLANNG
YGVSRILLEFTEDHSDNPTYLEREISETENLYKWLWKTNHPDAIQILLIGVICKKKH
LEYLSKASQKHPAAJIAAYATLLAIHEDKEWRKALVKLITATPELVCDVIPWYNAKAA
GILSECRPQSVAEECEYATVDMLPELLVSPPWMYKEKKNTPVFDLPVLEVPSYSDVT
                                                                                                                                                                                                                  PETTKKLTRTYLVTHFQQIAQQOATKQTLFTDLPPIKKASWEKHLIPLTPEGQILWHL
GEKRNRESGEKIYEKIPAPQSNUDALLREDFPALNAEFVHYHNAYKSWNLIALCYLP
GQQAISFLNOIUKENYSGEOLIIAIFGSAA.TPAFWACLQRDPRRLCFFPFFLGVSEL
ALPMAQQLQKKMSYEDARNWLIDYPRHAAAGLLPPALGKKGKDBCARQALRLIVNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                            ARKIKFKALQEHAREKINIYAENRGLTMAELEDRLAPDLGLDSSGSLILDEGPRKFTV
GFDETLKPVVCDANGKVLKDLPKPNQSDEKTQATDAVNLFKQLKKDVRAIASQOIDRL
EQAMCQRRRWTAEOFRLFLVEHPLVRHLTRRLLMGVYNDENALITCFRVAEDSTYSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSCSDEWADAISQAISLIKAQKTEIPARTWAVLTFLEICFCQGWNDETSSELLDEIVS
TFGIEXATETVIFWQIDDFDPYKDHLTFFINYADSSKDSYRRNNNKFSLERKKHLS
LABEEVWQNCIAKLLVALPDISLYRQPLIAILMPEIPEVAHEIVHRLHQVADVPQLEM
LKLVATDPFTLEILENYQYIDVFNYGASWSATVLREQGIAALARLTPYAEEDNCGDV
LKCINHPLAITNKKCRKFSFCNDSGISRSIGKKR"
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/protein_id="AAG57179.1"
/db_xref="G1:12516334"
/translation="MALAEALVKKDDKRKHTLLVSLLNANPLFVEKLVIGLSSQAANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSDIALMQINGIAQKLKFKALQERAKXKIAGIAESRELTVAELEDRLAPDLGLDDNGS
LLLDFGSRQFTVSFDETLKPFVRDVSGSRLKDLPKPNKSDDESQANDAVNRYKLLKKD
ARTVAAQQVARLESAMCLRRRWSPENFQLFLVEHPLVRHLTRRLIWGVYSTENQLLTC
                                                                                                                                                                                                                                                                                                                                                  QRETIEEIAQGYNQPDVLAALATLFDSDPLEEYPAKIAPLPGFYQFTLMRRPRLKSNN
LPLSDDAMRHLGTMLSFPRDITAYAGLDIIREIFTRESLAEFGWDLYPAWTEAGAPAK
ENWAFTSLGILGNDDTARKLTPLIRAWPGESQHKRAVSGLDVLADIGSDVALMLLNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELTRWQGRLCQAGRIVGLERRGWQRLEESGSVYAMRKTTPHGDLELETEPFSLIYGE
TGYGDQHPVESVKITSPDDRYGKQSSLTFSMLDDITASELINDIESLFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKTYIYQDEKSHKFWAVEQQGNELHINWGKVGTNGQSQVKSFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAEKAALKLIAEKVKKGYVEQVDANAHSHDASAKKVLVTEEKASINRQAATNGLPW
LADNDPIILPPNIARHALSHRLWPGEPVKKPTKPEKQNLISRLANRTYHYYKNLTFDY
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PLWTRPKLKNSSKVLPDSALOHLGEMLRFPQEEALYPGLLQVKDACTADSLAEFAWDL
FTAWLTAGAPSKESWAFTALGVLGNDDTARKLTPLIRAWPGESQHKRATVGLDILAAI
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DRNSYALTEAERNASELTRWAGRKCPSGRVWGLANKGWIKGTPQDGGWIGWMIKPLGR
WSLIMEIDEGFAVGMSPAELSAEQILSKLWLWEGXAESYGWGSNSTQEAQFSVLDAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDELFTLPAGNIGIPHVLEISPESAAAFRQIYADYELLPPFQQLERGSYHLADNERNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carriers: Molybdopterin"

Antoe"Residues 100 to 402 of 426 are 43.03 pct identical

to residues 5 to 309 of 1210 from Escherichia coli K-12

Strain MG1655: B2118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Residues 265 to 579 of 579 are 94.92 pct identical to residues 19 to 333 of 333 from Escherichia coli K-12 Strain MG1655: B2117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="putative regulator; Biosynthesis of cofactors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="putative regulator; Biosynthesis of cofactors,
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/protein_id-"AAG57178.1"
/db_xref-"GI:12516333"
regulator (fragment)"
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/transl_table=11
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/gene="molR_C"
/note="23285"
3923. .5203
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/gene="molR_D"
/note="23286"
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/gene="molR_C"
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/gene="molR_D"
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/note="23287"
6918. .10547
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gene

CDS

gene

CDS

1597 44

gene

CDS

32523

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misc_feature
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DB:
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KEYWORDS
SOURCE
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Mus musculus chromosome UNK clone RP24-326N11, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 157377)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                1383 GCATAAGCCGCAATAGCCGCAGCGGGATGCTTTTGACTGGCCTTGCTTAAGTATTCCAGG 1324
                                                                                                                   85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104
                                       65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
                                                                                                                                                                                                                                                                              ....-----MetLeuGluThrValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
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Contact: submissions@watson.wustl.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 178000; agarose-fp
Insert size: 158206; sum-of-contigs
Quality coverage: 13.54 in 020 bases; agarose-fp
Quality coverage: 13.67 in 020 bases; sum-of-contigs
                                                                                                                                                                                         105 ThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys----
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Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads.
Assembly program: Phrap; version 0.990319
Consensus quality: 156063 bases at least Q40
Consensus quality: 156847 bases at least Q30
Consensus quality: 157390 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
1596 ATCCAGGGCGGCGAAACAAGCAGCTCCGGCAAC-
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                                                                                                                                                                                                                                                                                                                                                                                   1323 TGCTTTTCTTACCAATTACACCGAGG 1297
                                                                                                                                                                                                                                                                                                                                                        AlaPheIleValProThrThrArg 134
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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AC124403 2431098 bp DNA linear HTG 20-JUN-2002 Mus musculus chromosome UNK clone RP24-36916, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49807 TTTGTCTGTATAGCA-----CCTGTCCCAGTTGTTTCCTACTGTCACCTTGATTCAAGA 49754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 TrpLyslleAlaAlaMetLysLeuSerSerGluSerLysAlaLyslleSerGluThrAla 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla
soon as it is available and the accession number will
                                  1149: contig of 1149 bp in length 1249: gap of unknown length 4356: contig of 3187 bp in length 4536: gap of unknown length 10728: contig of 6192 bp in length 10828: gap of unknown length 22669: contig of 11841 bp in length 22769; gap of unknown length 34710: contig of 11941 bp in length
                                                                                                                                                                                                        34810: gap of unknown length
157377: contig of 122567 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 others
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25
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AC124403.1 GI:21426522
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                      4537. 10728
/note-"assembly_name:Contigl3"
10829. 22669
/note-"assembly_name:Contigl4"
22770. 34710
/note-"assembly_name:Contigl5"
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34811. 157377
/note="assembly_name:Contig16"
34599 c 36427 g 43883 t
                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig5"
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Matches:
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                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
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                                                                                                                                                                                                                                                                                                                                            /clone="RP24-326N11"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.86e+03
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40.96%
30.12%
12.65%
  as soon as it
be preserved.
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                                                      1150
1250
4437
4537
10729
10829
22670
22770
34711
34811
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Best Local Similarity:
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Search completed: May
Job time: 2107 secs
       misc_feature
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                                                                                                                                                  McPherson, J. D. and Waterston, R. H.
McPherson, J. D. and Waterston, R. H.
Submitsed (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 243098)
McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 243098)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer ET: 08 of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 238434 bases at least Q40
Consensus quality: 238425 bases at least Q30
Consensus quality: 238425 bases at least Q30
Insert size: 178000; agarose-fp
Insert size: 242198; sum-of-contigs
Quality coverage: 17.40 in Q20 bases; sqarose-fp
quality coverage: 10.31 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of unknown length
contig of 107231 bp in length
app of unknown length
contig of 83148 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 4893 bp in length
gap of unknown length
contig of 12030 bp in length
gap of unknown length
contig of 12206 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 1312 bp in length
gap of unknown length
contig of 1105 bp in length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 14283 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...... Summary Statistics -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3723: contig of 3723 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown length
contig of 2267 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                               ---- Genome Center ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .243098
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/db_xref="taxon:10090"
/chrcmosome="UNK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Ml3; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6190:
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  Mus musculus
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ORGANISM
                                                               REFERENCE
AUTHORS
TITLE
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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Db 145256 GGTTAGACGGTCTCTCTCCATTCTGCTTCAGCATAAGTTGGGGCCACAGGTGACACTGCA 145315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGltThrAla 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysH1s 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 AlaValLysGlnThrCysGlnThr------GlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla
                                                                                                                                                                                                                                                                                                                                                                    901 others
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Matches:
Conservative:
Mismatches:
Indels:
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30.12%
12.65%
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Best Local Similarity:
Query Match:
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5, 2003, 22:28:35; Search time 43 Seconds (without alignments) 955.690 Million cell updates/sec
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1 MMKILYVTATLMTAFTLASC.....SLKPCMLETVNAFIVPTTTR 134
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                   OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                            441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                            Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		e Match Length DB	5857	3823	2324	12588	894	894	894	894	920	920	920	920
æ	Query	Match	13.1	12.6	11.4	11.4	11.3	11.3	11.3	11.3	11.3	11.3	11.3	11.3
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4 4 4 4 4 4	N 4 4 4 4	U 4 4 4 4 4	• • • • • • • • • • • • • • • • • • • •	448421311
920 920 920 2179 4291 439	1712 1712 1080 2574 6321	6749 6749 14187 5515 5519	24990 24990 24990 24990 24990 2214	2793 2793 4565 6756 6756 6756 2702 3744
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13 14 15 16 17	19 20 21 22 23	225 225 237 287	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	28 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
	0 0 0		000000	00 000

ALIGNMENTS

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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPRRATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: ROCKVILLE STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
                   Sequence 28, Application US/08961527; Patent No. 6420135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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US-08-961-527-28/c
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                                                                                                                                                                                                                                                                                                                                                                                                                           95 ThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHis 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                       58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla---LysIleSerGluThr 76
                                                                                                                                                                                                                                                                                                    5016 AATGAAAATGATAACCTTACGTCCAAGCAAATTAAATTCATAGATGCCATGCTTACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGlu-----Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4836 ACAACTCAAATGCTTTATTTAGCATCATCTAACGCTGTTTCTGTACTCAATGATATTATG
                                                                                                                                                                                                                                                                                                                                       43 ---AlaValLysGlnThrCysGln------ThrGlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                    Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                      30 AsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis--
                                                                                                                                                                                                                                     US-10-048-196-2 (1-134) x US-08-961-527-28 (1-5857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                    Indels:
                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blattner, Frederick R.
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 132, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicole T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burne, Nice
Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
5857 base pairs
                                                                                                                 0.747
88.50
48.54%
27.18%
13.09%
                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| ||| ||| 4716 TCTTATAAG 4708
                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WI
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                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-453-702B-132/c
                 ; TYPE: nuclei(
; STRANDEDNESS:
; TOPOLOGY: 111
US-08-961-527-28
                                                                                                 Alignment Scores:
 LENGTH:
                                                                                                                   Pred. No.:
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GTAATCAGTTTGACAAGCGCTTTACGCCACTCTTTATCTTCATGTATTGCCAGCAAAGTA 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Murison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysGlnThrCysGlnThrGlnLeuThrGlyH1sGlnTyrTrpLysIleAlaAlaMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHi$AláVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 LeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys
                                                                                                                                                                                                                                                                                                                     3823
33
22
65
39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-048-196-2 (1-134) x US-09-453-702B-132 (1-3823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1342 ATCCAGGGGGGGAAACAAGCAGCTCCGGCAAC-----
                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
960296.95017
                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILLNG DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/724,864 CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1069 TGCTTTTCTTACCAATTACACCGAGG 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AlaPheIleValProThrThrArg 134
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                   0.94
85.50
36.918
22.158
12.658
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                                                                                                                              LENGTH: 3823
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 -----
                                                                                                                                                                                                                                                         US-09-453-702B-132
                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TCCACAAACATTAAAATCCAAGAGGTG 2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2150 GGTTGCCACTGTGGTGGAGACAGATGCTCCCTCCCGTGGCCCATGGGCTTCTCTTGGTCT 2209
                                                                                                                                                                                                                                                                                                                                                2045 ACTTAGGAGGGGAGTACATGCAATCTGTCGGTAACATGAGGAAGTGCTCAACCTCACGAC 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 TyrTrpLys1leAlaAlaMetLysLeuSerSerGluSerLysAlaLys1leSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                           12 MetThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSer 31
                                                                                                                                                                                                                                                                                                                                                                                                         ---IleLysHisAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ERIESYAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BREK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STRRET: P.O. BIOX, 77
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2210 TCATGCCCTGAGGGGTTGGGGCTAACTGGTGTAGTCTTCGCTGTGG 2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIle 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 -----ValLysGlnThrCysGlnThrGlnLeuThr-----
                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                  US-10-048-196-2 (1-134) x US-09-724-864-21 (1-2324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1809-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AlaCysGlyCysValAlaAspLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08387942C Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                                         32 SerAlaAsnLeuThrThrSerLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MRRHY JR. GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2105 TCCTGGAAGCCTGCACTT-----
                                                                                                                                         5.41
77.00
37.93%
23.28%
11.39%
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                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                   TYPE: DNA
CRGANISM: Mouse
US-09-724-864-21
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SEQ ID NO 21
LENGTH: 2324
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APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: MULTIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 11525 ACGGCAACTTCGTCGGCCAGTTCAACGATGGCAACCTGTTGTTCGACGCCGCTCCGGTCA 11584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ACC 11608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 11729 CCGGGGCGGACGTGTTCCGCTTCGAGGCGCTGTCCGACAGCCCAGCGCAACTACACCGCCG 11788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11609 TGTCCGGCACCGATGCCGGGGAAACCTCCTGGGCTACGGCGACACGACACACCTCAACG 11668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 ProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSer 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsn 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 11789 GCGACAACCAGGGCGATTACATCGACTTCGCCGTGGGCGAAGACA 11836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 SerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-048-196-2 (1-134) x US-08-387-942C-1 (1-12588)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 GluSerLysAlaLysIleSerGluThrAla---
                                                                                                                                                                                               ORGANISM: Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 28, Application US/08467963C; Patent No. 5968776; GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 12588 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLGY: linear MOLECULE TYPE: DA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.21% 25.86% 11.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
9973..12588
                                                                                                                                                                                                                                                                                                                             CDS
2227..6438
                                                                                                                                                                                                                                                                                                                                                                                               CDS
6702..9695
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                    STRAIN: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-467-963C-28
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-387-942C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                        FEATURE:
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No
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APPLICANT: KLEIN, Michel H
APPLICANT: DU, Kun-Pan
APPLICANT: DU, Kun-Pan
APPLICANT: WASYSHYN, MATY E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
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34
21
53
53
53
      --AACCACAAACAAACCAATAATGATTTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      3, Application US/08838189D
5998169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-11E
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.44%
25.00%
11.32%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                 Toronto
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                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 6t
                                                               RESULT 6
US-08-838-189D-28
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                                                                                                           ; Sequence 28,
                        461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 CTTGGAATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 TCAACAACACCCAGGAGTCAAGTCAAACCTGCAACCCACAACAGTCAAGACTAAAAACACA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrThrAlaAlaIle-AsnPro-------AsnAlaArgThrGluValAl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 LysHisAla-----ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 TrpLyslleAlaAlaMetLysLeuSer....-SerGluSerLysAlaLysIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION UNDBER: US 08/838,189
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-78N-1993
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-78N-1993
APPLICATION NUMBER: CB 920017.1
FILING DATE: 06-78N-1993
APPLICATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEFHONE: (416) 595-1155
TELEFHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARAPERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-08-467-963C-28 (1-894)
3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
          STREET: 6th Floor, 330 Univers
CITY: Toronto
STATE: Ontario
COUNTX: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
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25.00%
11.32%
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
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US-08-467-963C-28
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133 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 192
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1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20
                                                                                                                                                                          21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle 40
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58 TrpLysIleAlaAlaMetLysLeuSer-----SerGluSerLysAlaLysIleSer
                                                                             GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu
                                                                                                                                                              ThrThrAlaAlaIle-AsnPro------AsnAlaArgThrGluValAl
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APPLICANT: DU, Run-Pan
APPLICANT: DU, Run-Pan
APPLICANT: EMASYSHYN, MAIY
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
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Conservative:
Mismatches:
Indels:
Gaps:
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REGISTRATION NUMBER: 24,973
REFERENC-ZOCKET NUMBER: 1038-688 MIS:jb
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6th Floor, 330 University Avenue
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APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                            US-08-852-344D-28; Sequence 28, Application US/08852344D; Patent No. 6017539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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25.008
11.328
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CITY: Toronto
STATE: Ontario
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Pred. No.:
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                                                                                                                                                        21 AlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle 40
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                                                 1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20
                                                                                                                                                                                                                                                             41 LysHisAla------ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 GluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeu 94
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TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
CORRESPONDENCE: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 ------AACCACCAAACAAACAAACAATGATTTCACT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
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APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14-NOV-1994
CLASSIFICATION: 424
US-10-048-196-2 (1-134) x US-08-852-344D-28 (1-894)
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330 University Avenue, 6th Floor
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
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APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 424
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Patent No. 6033668
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein, Michel H
Du, Run-Pan
Ewasyshyn, Mary E
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floor
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APPLICATION NUMBER: US/08/467,963C
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-08-344-639E-28 (1-894)
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Indels:
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                      Length:
Matches:
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Patent No. 5968776
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APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, Mary E
             TELEX: 065-24567 SIMBAS INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
(416) 595-1163
                                                                     LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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76.50
40.44%
25.00%
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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COUNTRY: Canada
ZIP: MSG 1R7
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Best Local Similarity:
                                                                                                                                              US-08-344-639E-28
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APPLICANT: KLEIN, Michel H
APPLICANT: DU, RUn-Pan
APPLICANT: EMASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               920
34
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Mismatches:
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                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1038-474 MIS: jb
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                                                                           APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
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                                                                                                                                                                                                                                           24,973
                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
                                                             FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                        1: 920 base pairs
nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.44%
25.00%
11.32%
                                                                                                                                                                                                                      NAME: STEWART, Michael REGISTRATION NUMBER: 2
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Best Local Similarity:
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US-08-838-189D-7
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108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr 123
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                                                                                                                                                                                                                        APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, MARY
TITLE OF INVENTION: CHIMERI
TITLE OF INVENTION: SYNCYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Sim & MCE
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTAGCCTCG 199
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                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                              E: Sim & McBurney
6th Floor, 330 University Avenue
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APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/838,189D
FILING DATE: 16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPANE: (416) 595-1155
TELEPANE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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25.00%
11.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                           CORRESPONDENCE ADDRESS: ADDRESSE: Sim & MCE
                                          NUMBER OF SEQUENCES:
                                                                                                                                         STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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  TITLE OF
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140 ATTCTGGCAATGATAATCTCAACTTCACTTATAATTACAGCCATCATATTCATAGCCTCG 199
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                                                                                                                                                                                                          TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
NUMBER OF SEQUENCES: 37
CORRESPONDENCE
---AACCACAAACAAACCAATAATGATTTTCACT 500
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34
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/852,344D
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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6th Floor, 330 University Avenue
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9200117.1 FILING DATE: 06-JAN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  Sequence 7, Application US/08852344D Patent No. 6017539 GENERAL INFORMATION: APPLICANT: KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
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Pred. No.:	Percent Simi Best Local S Query Match: DB:	US-10-048-19 Qy 1 ME	Db 140 AT Qy 21 AI	Db 200 GC	Db 236 CP Qy 58 Tx	Db 296 CI	Oy 75 G1	95		Qy 108 ac	USOB467-99 USOB467-99 USOB40ENCE	; FILING CLASS
:::	Qy 58 TrpLysileAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer 74	Oy 75 GluthralacysGlyCysValalaaspLysalaProGlualaValSerLeuthrGluLeu 94	Qy 95 ThrThralaalaile-AsnPro	Oy 108 aGlnLysIleValArgHiSSerLeuLysProCysMetLeuGluThr 123	RESULT 12 US-08-344-639E-7 Sequence 7, Application US/08344639E	; FALENT NO. 9043008 ; GENERAL INFORMATION ; APPLICANT: Klein, Michel H	; APPLICANT: Du, Run-Pan ; APPLICANT: Ewasyshyn, Mary E : TITLE OF INVENTION: CHIMPERT DEGREEN WHICH CONFEDS	ROTECTIC ND RESPI	DENCE ADDRES	; STREET: 330 University Avenue, 6th Floor ; CITY: Toronto ; STATE: Ontario	TIP: MGG 1R7 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compactible COMPUTER: I	, MOLECULE TYPE: DNA (genomic) US-08-344-639E-7

Alignment Scores:

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CTTGGAATCAGCTTCTCCAATCTGTCTGAAATTACATCACAAACCACCACCATACTAGCT 355
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STATE: Ontario
COUNTR: Canada
ZIP: MSG IR7
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: DATA COMPUTER: US/08/467,969A
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
920
34
21
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28
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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LICANT: Du, Run-Pan
LICANT: Bwasyshyn, Mary E
LE OF INVENTION: Chimeric Immunogens
BER OF SEQUENCES: 21
BESONUENCE ADDRESS:
DRESSEE: Sim & McBurney
PREET: 330 University Avenue, 6th Floor
                                                                                                                                       196-2 (1-134) x US-08-344-639E-7 (1-920)
                                                                                                  Gaps:
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5.: 6168786
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Similarity:
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355
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-08-467-969A-7 (1-920)
                          1038-475 MIS:bh
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330 University Avenue, 6TH Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrThrAlaAlaIle-AsnPro-----
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Patent No. 6171703
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic)
US-08-467-969A-7
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40.44%
25.00%
11.32%
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                       Alignment Scores:
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US-08-467-961A-7
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                 PatentIn Release #1.0, Version #1.25
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Mismatches:
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Matches:
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      SOFTWARE: Pateuth...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,961A
                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                        GB 9200117.1
PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Query Match:
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Mismatches:
Indels:
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                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
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Matches:
              APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    SOFTWARE: FEGENIN RELEASE #1.0, VEES
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,554A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELEFAX: (416) 595-1163
TELEEX: 065-24567 SIMBAS:
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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76.50
40.44%
25.00%
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TYPE: nucleic acid
STRANDEDNESS: single
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SENERAL INFORMATION:
                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity:
Query Match:
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1426 TTGAGGAAGTTCTTCTTTCTCAGAGCTACGTTAAAATGTATAACAAAGCTGTCAAGCTGT 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIle-AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysG 79
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                                                                                                                                                                                                                                                                                      APPLICANT: DOUGS, MACHAGEL D.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF I
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FEALSEQ for Windows Version 3.0
SECIED NO 152
                                                     500
                                 108 aGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 Cys---MetLeuGluThrValAsnAlaPheIleVal 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ndels:
                                                                                                                                                          Sequence 152, Application US/09370838 Patent No. 6444425
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US-09-351-200-1
; Sequence 1, Application US/09351200
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76.50
40.918
25.328
11.328
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael
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                                                                                                                                    US-09-370-838-152
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97 AlaAlaIleAsnPro 101
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Best Local Similarity:
Query Match:
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                                                                                                                                                                LENGTH: 439
                                                                                                                                              SEQ ID NO 98
                                                                                                                                                                                                                                                                                    Pred. No.:
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1685 GCTACAAGCAGCTCCTCAACTACTTTTATAGAACTGCTTCCATTAATGGTTTT 1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 ValSerLeuThrGluLeuThrThrAlaAlaIleAsn-----ProAsnAlaArgThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsn 125
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APPLICANT: BOURBONNAIS, YVes
APPLICANT: BOURBONNAIS, YVes
APPLICANT: DANARE, Claude
APPLICANT: DESLAURIERS, No. 63200331a
APPLICANT: DESLAURIERS, No. 63200331a
TITLE OF INVENTION: CANDIDA ALBICANS GENE (CSA1) ENCODING A
TITLE OF INVENTION: MYCELIAL SURFACE ANTIGEN, AND USES THEREOF
FILE REFERENCE: 6013-71"US CC/
CURRENT APPLICATION NUMBER: US/09/351,200
CURRENT APPLICATION NUMBER: CA2,237,134
EARLIER PILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
LENGTH: 4291
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
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; Sequence 98, Application US/09060756
pretent No. 6183957
; GENERAL INFORMATION:
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75.00
41.50%
24.49%
111.09%
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; LOCATION: (0)...(0)
US-09-351-200-1
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Best Local Similarity:
Query Match:
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APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PALENTIN VEI. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GCCACCCTGGCCGAAAGCTCGACA 424
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Sequence 1, Application US/08632598
Patent No. 5866164
GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
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24
17
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Mismatches:
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                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-98
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APPLICATION NUMBER: US/08/632,598
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NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
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48.24%
28.24%
10.95%
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1217 GAGATGTTGAGGTCGTTGATGATCACCGCCACAGCCGGACGTCCGCCTCCACC 1158
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APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
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43
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
223355/SEE50112/US
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             TELECOMMUNICATION INFORMATION: TELEPHONE: 861-3000
                                            TELEFAX: 822-0944
TELEEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                       TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: MUSA
IMMEDIATE SOURCE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                               51.43%
26.67%
10.95%
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Query Match:
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1217 GAGATGTTGAGCTTCACGTCGTTGATCACCGCCACAGCCGGACGTCCGCCTCCACC 1158
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Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037 CTCGTCCGGCTCGTCGCTAAGAAACTCGTGGTGAACTCCTCGTCTCCCCAACATGGAAGCG 978
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                            223355/SEE50112/US
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ADDRESSEE: Bayer Corporation
US/09/231,240
                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/632,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 661-3000
                                                                                                                                                                                                                                                                           TELEFAX: 822-0944
TELEX: 6714627 CUSH
INDORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 18
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74.00
51.43%
26.67%
10.95%
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: MUSA
IMMEDIATE SOURCE:
CLONE: ACS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: lines
MOLECULE TYPE: CI
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-231-240-1
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784 GAGCCGCGGGGCCTCGCTGGGCCCGCGTTCAGCACTTCTCGAGAGCCTGCTGGTGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCACGACCACTGCCGCGCTCGGGTGCGTC---GACAGCGCGCGCGGCGACGCCACGTG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLys-----HisAla 43
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                                                                  ZIP: 15205-9741

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1080
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22
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                    APPLICATION NAMER: PCT/EP97/00729,
APPLICATION NAMER: PCT/EP97/00729,
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERLSTICS:
LENGTH: 1080 base pairs
                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Parapox ovis
STRAIN: D1701-HD1R-Genregion
SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09255829 Patent No. 6461617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
 100 Bayer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCGGTAGCGCGGATGC-----
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
STREET: 100 Bayer RC
CITY: Pittsburgh
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.50
45.93%
29.63%
10.87%
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                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ValLysGlnThrCysGlnThr-----GlnLeuThrGlyHisGlnTyrTrpLysIleAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
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                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                     Version #1.30 (EPO)
             APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAspLysAlaProGluAlaValSerLeuThrGluLeuThr
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|TGGTCAGAACAAAGCAATCAACAAACAAGCTTACG----
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APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: PATENTIN Release #1.0, VCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
Clifford Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2574 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                      CORRESPONDENCE ADDRESS
                                                                   NUMBER OF SEQUENCES:
                                                                                                                                        CIT1.
STATE: D.
COUNTRY: USA
TO: 20005-3934
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Best Local Similarity:
Query Match:
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US-09-255-829-28
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                                                                                                                                                                                                                                                                                                                                                                                                           2320 CCAGAGGAAAAGCACATCTTCACGTGTAACCTTCAGATCGTGAGCTTGCTGGAGCATTTC 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2380 AGATATCTGAGCCATATTAGCACGACGAGCCACACCCCACTACTGCACCGCCACGATTCAC 2439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 rGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLys----Al
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                                                                                                                                                              US-10-048-196-2 (1-134) x US-09-221-017B-311 (1-6321)
                                      Mismatches:

    Curtis, Morris & Safford, P.C.
    Fifth Avenue

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions and Uses 190
                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2720.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
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FILING DATE: 05-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pincus, Steven E.
Cox, William I.
Kauffman, Elizabeth K.
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                                                                                                                                                                                                                                                                                                                                                    24 ProGlu-SerAsnProLysAsn--
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      45.79%
27.10%
10.80%
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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APPLICANT: Kauffman,
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-08-658-665-71/c
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STREET: 53
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APPLICANT:
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                                                                    Query Match:
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                                                                                                    1319 TCAAAGCACCGGGTATCTGCATCGACGTTGACAACGAAGACCTCTTCTTCATCGCAGACA 1378
                                                             96 ---ThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHis 114
                                                                                                                                                                                                                                      1439 ACTACATCGAAAACGACTTCCCGATCAACGAACTCATCCTCGACACGGACCTCATCA 1495
                                                                                                                                                                                     115 SerLeuLysProCysMetLeuGluThrValAsnAlaPheIleValProThrThr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6321
29
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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Patent No. 6444799
GENERAL INFORMATION:
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STREET: 755 PAGE MILL ROAD
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
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FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98,
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DNA (genomic)
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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COMPUTER READABLE FORM:
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STATE: CA
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                                                                                                                                                                                                                                                                                                             RESULT 23
US-09-221-017B-311
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Pred. No.:
Score:
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SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,7028
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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Burland, Valerie
Perna, Nicole T.
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INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS: LENGTH: 6749 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECHIP
                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-09-085-273-71
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23.85%
10.80%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                              18 AlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThr 37
                                                                                                                                                                                                                                                                                                                                                                                                       56 ....----GlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 Lys11eSerGluThrAlaCysGly-CysValAlaAspLysAlaProGluAlaValSerLe 91
                                                                                                                                                                                                                                                                                                                           38 SerLeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis----
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                                                                                                               Conservative:
Mismatches:
Indels:
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APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Kauffman, Elizabeth K.
TITLE OF INVENTION: RECOMBINANT POXVIRUS - C
TITLE OF INVENTION: COMPOSITIONS AND USES
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
                                                                          Length:
Matches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Curtis, Morris & Safford STREET: 530 Fifth Avenue CITY: New York STATE: New York COUNTRY: United States of America 21P: 10036
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,014
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 eValArgHisSerLeuLysProCys 119
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Patent No. 6267965
GENERAL INFORMATION:
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73.00
39.45%
23.85%
10.80%
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                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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                                                          Alignment Scores:
                  US-08-658-665-71
                                                                          Pred. No.:
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1814 TCGTCGTCGCCCTGGGCGCACCCTCGTCGTGCCGGTCCCAGGTGTGTCGGTACTCAAGC 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 ------GlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LysIleSerGluThrAlaCysGly-CysValAlaAspLysAlaProGluAlaValSerLe 91
                                                                                                                                                                                                                                  18 AlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThr
                                                                                                                                                                                                                                                                                                                                          38 SerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHis----
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ZIP: 53701-2113
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
6749
26
17
45
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TITLE OF INVENTION: No. 6365723el Sequences of NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                           Matches:
Conservative:
                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-09-085-273-71 (1-6749)
                                                                            Mismatches:
Indels:
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                          CURRENT APPLICATION DATA:
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72.50
45.198
29.638
10.728
                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ThralaThrLeuMetThr---AlaPheThrLeu---AlaSerCysAlaSerThrProGlu 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6834 TCTCGTAACGAATCCATATTCCCTAAATACAAACATGATTCCAAGCCTTGTGCAATA 6890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 GlnThrCysGlnThrGlnLeuThrGlyHis-----GlnTyrTrpLysIleAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-048-196-2 (1-134) x US-09-453-702B-121 (1-14187)
                                                          NAME: Seay, Nicholas J.
REGISTATION UNDRER: 2736
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
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STREET: 100 Bayer Road
CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                   TELEPHONE: (608) 251-5000
TELEFA: (608) 251-9166
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                  FILING DATE: 04-DEC-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6759 ATCACAAAATCTTCG------
                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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42.028
29.418
10.808
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                                                                                                                                                                                                                      LENGTH: 14187
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Best Local Similarity:
Query Match:
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891 AGCAACGCGACTTCGCGCTCGCAGTCGGCGACGAA-GCCCTCGTGAAGACGGCGCACGGC 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 -----LeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  667 GTTGCGTTTGACGAGCATGTTCGAGATCGGTGTGCGTCCGGCGGCTGACACGACGGTGGG 608
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US-09-125-642C-12/C
US-09-125-642C-12/C
Sequence 12, Application US/09125642C
Patent No. 6365393
GENERAL INFORMITION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a)
TITLE OF INVENTION: Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 aLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSer--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 ValLys---GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr-TrpLysIleAlaAl
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                               Fragment I (Version 1) NO: 8:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                 FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00729,
FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5515 base pairs
                                             APPLICATION NUMBER: US/09/125,642C
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Parapox ovis
STRAIN: D1701- HIND III
SEQUENCE DESCRIPTION: SEQ ID
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Betlach, Mary C.

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954 TCCTTGCTGACCAGCACGACCAGCGCGCTCACGGCCGGTGTGCCGAGCATGCTGCGGGAA 895
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NOMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu1leLys---
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Parapox ovis
STRAIN: D 1701, HindIII-Fragment I,
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                          APPLICATION NUMBER: PCT/EP97/00729,
FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5519 base pairs
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
Pennsylvania
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72.50
45.19%
29.63%
10.72%
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DB:
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 LeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThr
APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
TITLE OF INVENTION: THERREPOR
FILE REFERENCE: 30062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
EARLIER APPLICATION NUMBER: 099-31
EARLIER APPLICATION NUMBER: 09/010,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28696 CACGAGAAAGGCAGCAGCACGTCGCCGCGCTGATACCTCCGCAAACGCTGCGA 28643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 -------GluThrValAsnAlaPheIleValProThrThrArg 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GlnLysIleValArgHisSerLeuLysProCysMetLeu--
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                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
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Shenbagamurthi, Ponniah
Culler, Michael D.
Setcavage, Diane R.
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; GENERAL INFORMATION: APPLICANT: APPLICANT: Harris, Crafford A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldstein, Gideon
Siekierka, John J.
                                                                                                                                                                                                                                                                                   ORGANISM: Sorangium cellulosum US-09-144-085-3
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72.00
36.96%
26.81%
10.65%
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity:
                                                                                                                                                                                                                                               LENGTH: 33529
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US-08-171-382-1/c
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APPLICANT:
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                                                                                                                                                                                                                               SEO ID NO 3
                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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Query Match:
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30
18
41
22
           STREET: Spring House Corporate Cntr, P.O. Box 457 CITY: Spring House STATE: Pennsylvania
                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,382
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTOREY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/POCKET NUMBER: IR143USA
TELECOMENUICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08309420 Patent No. 5591588 GENERAL INFORMATION:
                                                                        ZIP: 1947/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"AMPUTER: IBM PC COMPATIBLE
"O"-DOS/MS-
Howson and Howson
                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2490 base pairs
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71.50
43.24%
27.03%
10.58%
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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LOCATION: 205..2286
                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
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Best Local Similarity:
Query Match:
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US-08-309-420-1/c
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                                                             COUNTRY:
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Method for the Diagnosis of Depression
Based on Monitoring Blood Levels of Arginine Vasopressin
and/or Thymopoietin
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1838 GAAATAAACCCTAGGATTTCATCATCTATTTGGAACTGATAATATCTGTGTTGCCTCC 1779
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,420
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                           ADDRESSEE: Howson and Howson
STREET: 321 No. 5591588ristown Road, Box
CITY: Spring House
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                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MARY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR146
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 540-5207
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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71.50
43.24%
27.03%
10.58%
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STRANDEDNESS: double
                                                                                         CORRESPONDENCE ADDRESS
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LOCATION: 205..2286
                                                                    NUMBER OF SEQUENCES:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity:
                                                                                                                                                                                                         USA
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1613 GTGAGTGAATGAGAGACAGTTTTGGCAAAAGAAGACATCAGTTCGGATCCAGGTATG 1554
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      89 ValSerLeuThrGluLeuThrThrAlaAla-IleAsnProAsnAlaArgThrGluValAl 108
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                                                                                                                                                                                                                                     APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Method of Measuring
TITLE OF INVENTION: Thymopoietin Proteins in Plasma and Serum
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN Release #1.0, Version#1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11856
FILING DATE:
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Matches:
                                                                                                             1553 TTCTGAAATGCCACAAAGGAACCTGAATCCC 1523
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                                                                                  108 aGlnLysIleValArgHisSerLeuLysPro 118
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STREET: 321 Norristown Road, Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,419
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                        Sequence 1, Apjlication PC/TUS9511856
GENERAL INFORMATION:
APPLICANT: Immunobiology Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IRI45
FELECOMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2490 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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71.50
43.24%
27.03%
10.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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205..2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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STRANDEDNESS:
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1838 GAATAAACCCTAGGATTTCATCATCTATTGGAACTGATAATATCTGTGTTGCCTCC 1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAla 88
                                                                                                                                       APPLICANT: Goldstein, Gideon
APPLICANT: Goldstein, Gideon
APPLICANT: Goldstein, Michael
TITLE OF INVENTION: Method of Measuring Thymopoietin
TITLE OF INVENTION: Method of Measuring Thymopoietin
TITLE OF INVENTION: Method of Measuring Thymopoietin
TITLE OF INVENTION: Proteins in Plasma and Serum
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howeon and Howson
STREET: 31 No. 5593842ristown Road, Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-08-309-419-1 (1-2490)
1553 TTCTGAAATGCCACAAAGGAACCTGAATCCC 1523
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAK, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR14;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-506
TELEFAX: (215) 540-508
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                        US-08-309-419-1/c
; Sequence 1, Application US/08309419
; Patent No. 5593842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2490 base pairs
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27.03%
10.58%
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205..2286
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                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                           RESULT 32
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	1718 TCTTCTTCATTACTTTTAAAATAGATTCATGGAAGGAAAGGTAGTGTGTGTGTG	0y 89 %alserLeuThTGluLeuThTHTAlaAla-TieAanProAshArgThTGluValAl 108 bb 1613 GTGTGAAATGCCACAACATTTTGGTAAACACACACTTCGATCCGGTATG 1554 0y 108 addluLingthaATGHISEACHULYPED 118 bb 1553 TTGTGAAATGCCACAAACATTTTGGTAAACACACTTCGATCCGGTATG 1554 0y 108 addluLingthATGHISEACHULYPED 118 bb 1553 TTGTGAAATGCCACAAACACTGAATCC 1523 RESULT AND 1140 1 Sequence 14 Application Us/090108098 1 Setert No. 6005601 1 Sequence 14 Application Us/090108098 1 Setert No. 6005601 2 Sequence 14 Application Us/090108098 1 Setert No. 600562-20050 2 Sequence 14 Application Us/090108098 3 Setert No. 600562-20050 3 Setert No. 600562-20050 3 Setert No. 600562-20050 3 September Faterin Net. 2.0 3 September Septemb
Db 1718 TCTTCTTCAATTACTTTTAAAATAGATTCATGGAAGGGAAAAGATAGT 1671 Oy 69 SerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAla 88		PERSULT 34 PERSULT 34 PERSULT 34 PERSULT 34 PERSULT 34 PERSULT 1898-1/2 PERSULT 34,7 PERSULT

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1183 TCTGCTTCAACTTCTCAGAAAAAGACCACAAATCTACGACATCTACACAAAGTAAAAGC 1242
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1243 AAAGTTACTTTATCTCCAACTGCAAGCGGCGCTATCAAACATCAAACTACAAGTACA
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83.AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla---IleAsnPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---MetLeuGluThr---ValAsnAlaPhe 127
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                                                                                       495 CTCACCCGGANCTCGCTCCCCCGTGCGTGCAACGCCACUTCCGAA 448
                                                         LeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGlu 106
                                                                                                                                                                                                                       TITLE OF INVENTION: IMMOBILIZATION AND PURIFICATION OF FUSION PROFEINS USING CHITIN-BINDING ABILITY
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/303,827
FILLING DATE: 30-JAN-1989
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Patent No. 573371
GENEZL INFORMATION:
APPLICANT: Lewis, Randolph V.
                                                                                                                                                                                                    APPLICANT: Kuranda, Michael J.
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Best Local Similarity:
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                                                                                                                                                                                   ; Patent No. 5258502
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                        CDNAS Encoding Minor Ampullate Spider Silk Proteins
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OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                                                                                                                           Version #1.25
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                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             IMBER: US/08/209,747
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGIGSRATION NUMBER: 28,977
REFRENCE/COCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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19.278
10.288
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69.50
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 14-MAR
APPLICANT: Colgin, Ma
TITLE OF INVENTION: C
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                         Virginia
                                                                                                                                                                                                                   22040-3487
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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ORGANISM: Nep
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GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                    US-08-776-265-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-776-265-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Cojgin, Mark
TITLE OF INVENTION: cDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2793
21
27
26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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Matches:
Conservative:
Mismatches:
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STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-08-458-298-1 (1-2793)
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Gaps:
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TISSUE TYPE: minor ampullate gland
                                                     1886 CTCCAGCAGCTGCCAGCACCAGCTC 1860
                                 108 AlaGlnLysIleValArgHisSerLeu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/458,298 FILING DATE: 02-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                Sequence 1, Application US/08458298
Patent No. 5756677
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2793 base pairs
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69.50
44.048
19.278
10.288
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STRANDEDNESS: double
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02 CLASSIFICATION:
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Best Local Similarity:
Query Match:
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ORGANISM: Ne
                                                                                                               US-08-458-298-1/C
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                                               2110 AGCTCCTGCAGCGGCTCCAGCACCAGCACCTAACGTAACCACCAGCGCCTCCGGATCC 2051
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                                                                                                                                                                                                                                                                                                                               88 AlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluVal 107
                                                                                                                                                                                                 68 GluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGlu 87
28 ProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThr 47
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APPLICANT: FAMECHON, Alain
APPLICANT: FERRERO, Lucia
APPLICANT: FERRERO, Lucia
TITLE OF INVENTION: No. 6001631e1 Topoisomerase IV, Corresponding
TITLE OF INVENTION: Nucleotide Sequences and Uses Thereof
                                                                                                48 CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSer
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/776,265
FILING DATE: 24-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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35.06%
21.43%
10.28%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CORRESPONDENCE ADDRESS:
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                                                                  1285 ACGTGTTTCATTTTTGTGACTTTTTTTTTACTTAACATAAATCAGCTTCCACTAAGACGCCC 1344
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                                                                                                                                                                                                                                                                                                                                                                                  ------MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly 79
                                          13 ThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSer 32
                                                                                                                                                                                                              ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAla-----
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APPLICANT: Annemarie E. Veenstra
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
ANNESSIONENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1525 ------ATTAGCACATTAATAATACTGACTACGACT 1554
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                                                                                                                            33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln.
US-10-048-196-2 (1-134) x US-08-776-265-2 (1-4565)
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: 545 Middlefield Road, Suite 200
Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert F.M. Van Gorcom
Willem Van Hartingsveldt
Petrus A. Van Paridon
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APPLICATION NUMBER: US/08/151,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H:
REJISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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STREET: 54
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AlaAlaIleAsnPro----AsnAlaArgThrGluValAlaGlnLysIleValArgHis 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 TyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr
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                                                                                                                                                                                                                                                         ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: lambda AF
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-08-151-574-31 (1-6756)
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/evidence= EXPERIMENTAL
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    24615-20026.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product= "Phytase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphatase"
                                                                                                                                                                                                                                                                                                                   LIBRARY: lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
                           IELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                         TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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356..1715
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210..253
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE
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NAME/KEY:
LOCATION:
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LOCATION:
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Pred. No.:
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6058 ACTIGGATACACCCGGAATCGAACGCAGTACTCCGTACGGCGAAAGTTTTCCTTTTGAAT 5999 g

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Search completed: May 5, 2003, 23:20:00 Job time : 66 secs

OM protein

Run on:

Seguence:

Title:

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Sequence 489, App Sequence 524, App Sequence 524, App Sequence 587, App Sequence 19149, A Sequence 152, App Sequence 152, App Sequence 1, Appli Sequence 121, App Sequence 121, App Sequence 121, App Sequence 121, App Sequence 28770, A Sequence 218, App Sequence 2249, App Sequence 2249, App Sequence 2249, App Sequence 51, Appli Sequence 248, Appli Sequence 248, Appli Sequence 249, Appli Sequence 51, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESSONDENCE ADDRESSE: Quarles & Brady STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26,
Sequence 46,
Sequence 46,
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MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                     US-09-738-626-2345
US-10-152-661-524
US-09-866-050A-524
US-10-1152-661-587
US-09-866-050A-587
US-09-864-761-19149
US-09-804-4727
US-09-804-133-152
                                                                                                                                                                                                  0. 05-09-738-973-152

0. 05-09-818-973-152

0. 05-09-818-914-1

0. 05-09-818-1

0. 05-09-815-242-9978

0. 05-09-972-186A-1

0. 05-09-978-1973-5

05-09-918-842-1071

0. 05-09-815-242-4580

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0. 05-09-815-242-8991

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0. 05-09-918-995-28770

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FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 132, Application US/10114170
Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burland, Vale
Perna, Nicole T.
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Welch, Rod
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ZIP: 53701-2113
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                                                                                                                                                                                                                                                                            STATE:
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-MODEL-frame+p2n.model-DEV=x1h
-MODEL-frame+p2n.model-DEV=x1h
-MODEL-frame+p2n.model-DEV=x1h
-MODEL-frame+p2n.model-DEV=x1h
-DB-PUDLished_Applications_NA -QFWT-fastap -SUFFIX*rnpb -MINNATCH=0.1
-DOPCCL=0 -LOOPEXT=0 -UNITS-Dits -START=1 -MATRIX*blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE=pct -THR_MAX=10
-THR_MIN-0 -ALIGN+40 -MODE-LCAL -OUTFWT=pto -NORM-ext -HEAPBIZE-500 -MINLEN=0
-MAXLEN=200000000 -USER=US10048196_@CGN_1].84_@runat_28042003_IS1442_5681
-NCPU-6 -ICOPU3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NGC_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1759.303 Million cell updates/sec
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                                                                                                                                                                                                                                                                               676
1 MMKILYVTATLMTAFTLASC......SLKPCMLETVNAFIVPTTR 134
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                               ; Search time 90 Seconds
                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                    - nucleic search, using frame_plus_p2n model
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US-09-815-242-8609
US-08-781-986A-447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    746064 seqs, 590810554 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA:*
                                                                                                                                                               5, 2003, 23:20:04
                                                                                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Database :

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Total number Minimum DB Maximum DB

Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1189 GTAATCAGTTTGACAAGCGCTTTACGCCACTCTTTATCTTCATGTATTGCCAGCAAAGTA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1129 GCATAAGCCGCAATAGCCGCAGCGGGATGCTTTTGACTGGCCTTGCTTAAGTATTCCAGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 ThrGluValAlaGlnLysIleValArgHisSerLeuLysProCys ----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TyrvalThrAlaThrLeuMetThrAlaPhe---ThrLeuAlaSerCysAlaSerThrPro 24
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
                                                                                                     NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-5166
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-048-196-2 (1-134) x US-10-114-170-132 (1-3823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 132: US-10-114-170-132
               APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               0.122
85.50
36.91%
22.15%
12.65%
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
ULE TYPE: DNA (g
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT:
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539 ATGCCACCAGTACATACGTAACC -- - ACTITITATCTGCAAATAACGCTTTATTCTCT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 TCTTCTTCTAAATCTAAAGCAACAATCTCTTTTCGAGGACGTACATGCATTTTCTTAAAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet-----Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 Ala---ProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                                                           of Essential Genes in
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                     APPLICANT I AGRAGATOR NO PER APPLICANT I AGRAGATOR I TITLE OF INVENTION: Identification of Essenti TITLE OF INVENTION: Identification of Essenti TITLE OF INVENTION: Identification of Essenti TITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001.03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8609, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus
                          amamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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45.30%
29.06%
12.43%
Carr, Grant
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.30%
29.06%
12.43%
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                           Maryland
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                           20850
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 ATGCCACCAGTACATACGTAACC---ACTTTTTATCTGCAAATAACGCTTTATTCTCT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 TTAATCCAGTCAGGCAAATCTCTAAAGCGCGTGATATTTGGACGAATTGCACCTCGGAAA 426
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKATYOUS
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PAPLICATION NUMBER: 06/19,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-20-16
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119
44
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8609
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; Sequence 447, Application US/08781986A
; Publication No. US20030054436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Staphylococcus aureus
                                                  Yamamoto, Robert T.
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45.30%
29.06%
12.43%
                                Carr, Grant
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Best Local Similarity:
Query Match:
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US-09-815-242-8609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AGAGCTTTTCTAAATTCTACAGGTGATAAATAFTGGCCAGTTGTGTGTGTTTTGGATCGACG 427
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                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-048-196-2 (1-134) x US-08-781-986A-447 (1-1799)
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Matches:
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                                                                                                              Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
                                                                                                           ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1936 GCATAGCATCCAAAGTTAAAAGGGTTGTGCAACTAGCTCGAGAGGAAATCAAGAATGGAA 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 leAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg-HisSerLeuLysPro 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
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                                                                                                                            APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Ramalakar
APPLICANT: Glukotta, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/92,849A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR PILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 sHisAlaValLys-----GlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 lyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996 AATGTGTTGTAATTGGTCTGCAGTCTACAGGAGAAGCTAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-048-196-2 (1-134) x US-09-822-849A-489 (1-2456)
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Indels:
Gaps:
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Matches:
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Sequence 489, Application US/09822849A Patent No. US20020045170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AlaSerThrProGluSer-----
                                                                                              Fechtel, Kim Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.455
79.50
41.56%
25.32%
11.76%
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
                                                        APPLICANT: Wong, Gordon G.
                                                                          Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-09-822-849A-489
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Best Local Similarity:
Query Match:
                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 489
LENGTH: 2456
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                            APPLICANT
                                                                                            APPLICANT
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57 TCCAGCAGTGATTCCTTTCGGAGTCAAGCACCTCTTCTTCCACCTCTTTCGGCTGCG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 LysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGlu-----ThrAla 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 CysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAla 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 TCTGATGCTGCGACTCAGTACCCAACTGCTGAGGAACTGAAT---------
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27
28
47
13
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES PERER RESE 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 99/317484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum -2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 524, Application US/10152661
Publication No. US20030022835A1
GENERAL INFORMATION:
                    MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Mathew APPLICANT: Onrust, Rene
SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.50
47.83%
23.48%
11.61%
                                                               HAYASHI, MIKIRO
                                                                                                                         TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                         YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: . Murison, James
                                                                                   OCHIAI, KEIKO
                                                                                                                                                                      IKEDA, MASATO
OZAKI, AKIO
                                        ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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SOFTWARE: Paten
SEQ ID NO 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-738-626-234
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                                                                                   APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 LysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPheIleVal 129
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PPLICANT: Kumble, Krishanand D.
ITLE OF INVENTION: Compositions Isolated From Skin Cells.
ITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980
33
20
53
16
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                     FILE KEFEKENCE: 1100.10110.10110.
CURRENT PELLING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-20
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 1900-07-25
PRIOR FILING DATE: 1900-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-10-03
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 725
SOFTWARE: PASLESEQ for Windows Version 4.0
SEG ID NO 5-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 524, Application US/09866050A
Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
                                                             ILE REFERENCE: 11000.1011c5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.448
27.058
11.548
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rat
US-10-152-661-524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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329 CCTACAGTG-----TCTCTTTCCCCATGTTTAGCAAGATCGCAGTCACTGGCACTGGTG 382
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PPLICANT: Kumble, Kirshanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
                                         APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 201-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
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Sleeman, Matthew
Onrust, Rene
Sleeman, Matthew
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                         Onrust, Rene
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Best Local Similarity:
Query Match:
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US-09-866-050A-524
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LENGTH: 980
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1934 GTGACTGCACCGGCAATTTCTGTTTGTTCAAGTCTACCA------CCAAGGACCTTC 1984
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
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Matches:
Conservative:
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Indels:
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              PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 1099-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-10-05
STORMARE: PASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 587
LENGTH: 2324
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CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 587
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APPLICATION NUMBER: 60/221,232
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Best Local Similarity:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIG
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Mismatches:
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-03
PRIOR PLILOR DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                0.964
77.00
37.93%
23.28%
11.39%
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Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 2324
TYPE: DNA
ORGANISM: Mouse
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                    Milne, Todd
No. US20020128250Alman, Thea
Sequence 427, Application US/09801368 Patent No. US20020128250A1
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                                      GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
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Best Local Similarity:
Query Match:
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LENGTH: 1818
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                                          APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FASLSEQ for Windows Version 3.0
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Conservative:
Mismatches:
Indels:
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Application US/09854133
D. US20020183499A1
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Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                            1.03
76.50
40.91%
25.32%
11.32%
                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapien
US-09-854-133-152
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APPLICANT: Reed, St.
APPLICANT: Henderso
APPLICANT: Lodes, M
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
Sequence 152, Applic
Publication No. US20
GENERAL INFORMATION:
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US-09-738-973-152
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LENGTH: 2179
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Patent No. US/2020/14/2417A1
GENERAL INFORMATION:
APPLICANT: Paigen, Beverly
Beier, David R.
TITLE OF INVENTION: of Use Therefor
                                                                                                                               APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEO ID NOS: 587
SOFTWARE: FASTSEQ for Windows Version 3.0
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Mismatches:
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Matches:
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                                Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
Fling, Steven P.
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76.50
40.918
25.328
11.328
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US-09-738-973-152
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Best Local Similarity:
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                                                                                               APPLICANT:
                                                          APPLICANT
                                                                           APPLICANT
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APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
APPLICANT: Charkowski, Amy O.
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 CCCAGCCTTAAGTCTTTGCGGAAATTGGGGCTGCATCTGCACATCCAGTACTGG----- 631
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                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/819,505
FILING DATE: 28-Mar-2001
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: JL-2001
                                               Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECONMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                       COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09825414 Patent No. US20020083489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1193 base pairs
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Farrell & PSTREET: P. O. BOX 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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74.50
50.00%
29.27%
11.02%
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Best Local Similarity:
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CITY: Brentford
STATE: CURNOwn>
COUNTRY: UK
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Publication No. US20030022321A1
GENERAL INFORMATION:
APPLICANT: SMithKline Beecham plc et al
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30365
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22
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26
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                         n at any position is undefined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-11-17
NUMBER: OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver: 2.1
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                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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42.28%
24.39%
11.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (29734)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                       30365
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                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                              LYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
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64 LysLeuSerSerGluSerLysAla-
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ORGANISM: Artificial Sequence
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Carr, Grant J.
Yamamoto, Robert T
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.48%
25.22%
10.80%
                          AMER, SANDRA W.
HUISMAN, GJALT
                                                            MILLIS, JIM
SHELDON, ROGER
                                                                                                DEL CARDAYRE,
                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION:
US-09-972-186A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-9978/c
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                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TGCTCTGTCCGTCGTTCTTCGGCCGGGACCACACCGGGT 4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 ValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPhelleValProThr 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LysileSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu
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                                                     COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
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Mismatches:
Indels:
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                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 08-Feb-2002
CLASSIFICATION: <u >CURROWN></u>
                                                                                                                                                                                                                                                        NAME: Valentine, Jill B
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: P31731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11near
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                   APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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US-09-972-186A-1
Sequence 1, Application US/09972186A
Patent No. US20020137153A1
                                                                                                                                                                                                                                                                                                                              TELEPHONE: 0181-9752000
TELEFAX: 0181-9756294
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7193 base pairs
                                                                                                                                                                                                                      FILING DATE: <Unknown>
ZIP: TW8 9EP
JTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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23.77\
10.87\
                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
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Best Local Similarity:
Query Match:
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APPLICANT: TOBIN, MATTHEW
APPLICANT: TOBIN, MATTHEW
APPLICANT: COX, ANTHONY
APPLICANT: COX, ANTHONY
APPLICANT: DAVIS, S. CHRISTOPHER
TILLE OF INVENTION: ENANTIOSELECTIVE PRODUCTION OF AMINO CARBOXYLIC ACIDS
CURRENT APPLICATION NUMBER: US/09/972,186A
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 -------CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description of Artificial Sequence: Synthetic nucleotide sequence
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Indels:
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Matches:
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Page 11

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SEQ ID NO 7375
LENGTH: 10429
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Publication No. US20030077808A1
GENERAL INFORMATION:
FAPPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEC ID NOS: 10231
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 ThralaalaileAsnProAsnAlaArgThrGluValAlaGlnLys 110
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Matches:
Conservative:
Mismatches:
Indels:
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                                  THILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-216
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PASLESEQ FOR WINDOWS VERSION 4.0
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45.26%
26.32%
10.80%
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ORGANISM: Salmonella typhi
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-764-891-7375/c
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US-09-815-242-9978
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Welch, Rod
TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                         8242 CTTCCCACCACCTCCATGTTGACAACAGGAACGGGACCCCCAGCAGTGAGCTCTGTCCT 8183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg 113
                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 SerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGlu 93
                                                                                                                                                                                                                                                                                                                4 IleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                8413 TCCACACATCCCCTCAGTCAATCCTCAAAACCATTGCCTGTGGAGGTAGTTATTATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                      24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETLE, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr. 2002
CLASSIFICATION: <Unknown>
                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x US-09-764-891-7375 (1-10429)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 121, Application US/10114170
Publication No. US20033075A1
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valerie
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Perna, Nicole T.
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                                                                                                          39
73.00
39.84%
26.02%
10.80%
TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-7375
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8131 TTTCCCTA 8123
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Percent Similarity:
Best Local Similarity:
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                                                                                        Alignment Scores:
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                                                                                                               Pred. No.:
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374 GCGGCAAGAACTTCACAAACTACGGCTCCGACCGTCTCCGGAGCAGCAGACTCATTCAAAA 433
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251 CTAATCACGCGCTTAACACGCATCACTCTGATTTCTGCTCCG------CCGCGGAAAC 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 SerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaVal
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-048-196-2 (1-134) x US-09-938-842A-1071 (1-1875)
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Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001.03-21
PRIOR PELLORATION NUMBER: 60/191,078
PRIOR FILING.DATE: 2000.03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELLORATION NUMBER: 60/207,727
PRIOR PELLORATION NUMBER: 60/207,727
PRIOR PELLORATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELLORATION NUMBER: 60/203,625
PRIOR PELLORATION NUMBER: 60/203,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1071 LENGTH: 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4580, Application US/09815242 Patent No. US20020061569A1
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-12-22
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                  ) ORGANISM: Arabidopsis thaliana US-09-938-842A-1071
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Zyskind, Judith W.
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72.00
46.59%
27.27%
10.65%
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Best Local Similarity:
Query Match:
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                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6759 ATCACAAAATCTTCG------ 6788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ThralaThrLeuMetThr---AlaPheThrLeu---AlaSerCysAlaSerThrProGlu 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6834 TCTCGTAACGAATCCATATTCCCTAAATACAAACATGATTCCAAGCCTTGTGCAATA 6890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 MetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAla
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                        RAME: Seay, Nicholas J.
REGISTATION UNBER: 27386
REFERENCE/DOCKET MUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 255-9166
INFORMATION FOR SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 121: US-10-114-170-121
                       FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
  APPLICATION NUMBER: 09/453,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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29.41%
10.80%
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APPLICANT: Kreps, Joel
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APPLICANT: Wang, Yun
APPLICANT: Zhu, Tong
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Best Local Similarity:
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SOFTWARE: Fast:
SEQ ID NO 8291
LENGTH: 7107
TYPE: DNA
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysVal----
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REPERBLOE: ELITRA.011A
CURRENT APPLICATION NUMBER: U5/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Obligan, Wari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawlick, John D.
APPLICANT: Trawnick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4580
                                                                                                                    29.8
72.00
39.64%
29.73%
10.65%
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                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                       Alignment Scores:
; SEQ ID NO 4580
; LENGTH: 7104
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6193 CCTGCAACAGAAGATAATGCAACGCCAGCAGAAAGCGCAACAATAACAATAGTACA 6252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43
                                                                                                                                                                                                                                                                                                                                                                                                            9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysVa≇----- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3:0
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Matches:
Conservative:
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Matches:
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Gaps:
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FastSEQ for Windows Version 4.0
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US-09-918-995-28770
                                                                            ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                              39.648
29.738
10.658
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40.00%
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LOCATION: (1)...(454)
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                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (1)...(7107)
US-09-815-242-8291
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                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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LENGTH: 454
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Db 846 AAGGGTCTTACC Qy 61 AlaAlaMetLysLeu bb 903 TCAGCAGTGCCTACA Qy 72LysIle		Db 1023 GTTAAAAGTACTCCT Qy 109 GlnLysIleValarg		Db 1131 CAGCCA 1136 RESULT 27 US-09-938-842A-812/C	GENERAL INCORMATION: GENERAL INCORMATION: APPLICANT: HATCH JOG HAPPLICANT: HATCH JOG TITLE OF INVENTION: STATE OF INVENTION OF STATE	Oy 47 ThrCysGlnThrGlr Db 621 Oy 67 SerGluSerLysAl8
st Local Similarity: 29.00% Mismatches: 43 ery Match: 10.58% Indels: 17 9 Gaps: 4 -10-048-196-2 (1-134) x US-09-918-995-28770 (1-454) 6 TyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGlu	Db 139 TGGGCAGCGGCTGCCGCATCGAATGCATATTCTTCAGCGAGTTCCACCCCAGGC 192 Qy 26 SerAsnPro	Oy 37 ThrSerLeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGln 56	Oy 57 TYTTPLYS	Oy 71 AlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSer 90 1	RESULT 26	Oy 29 LysasnSerSerAlaasn

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STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE P1300-3
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TIGCAGTCAACAGGAAATAAAGCAGAAGAACAAAAGGAACCGAATGT 1022
                                                                                                                                                                                                                                                :::|||:::||||
CTGTCACTTCTGCTGCAGATTCCT-----GAAGTAAAG 1070
                                                                                                                                                                 luLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAla 108
                                                                                                                                                                                                                           rgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPheIle 128
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GAAGCAGCATAACCTCCACCTCCTCCACCTCGGGAACC 661
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                                                                                                      leSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAla 88
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                                           euSerSerGluSerLysAla-----71
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2001-08-24
MBER: US 60/227,866
000-08-24
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2001-01-16
UMBER: US 60/300,111
2001-06-22
S: 5379
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71.00
39.37%
18.90%
10.50%
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Oy 109 nLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPhe 127	TCTCTTGGCAAACATTCACTCCTTT 1030	US-09-880-107-2249/c; :; squence 2249, Application US/09880107; Patent No. US20020142981a1; GENERAL INFORMATION:	APPLICANT: Horne, Darci T. APPLICANT: Vockley, Joseph G. APPLICANT: Scherf, Uwe APPLICANT: Gene Logic, Inc.	; TITLE OF INVENTION: Genbank Accession No. US20020142981al miles in Liver Cancer; FILE REFERENCE: 44921-5028-w0; CURRENT APPLICATION NUMBER: US/09/880,107; CURRENT FILING DATE: 2001-06-14; PRIOR APPLICATION NUMBER: US 60/211,379; PRIOR PELING DATE: 2000-06-14; PRIOR FILING DATE: 2000-06-10-02; NUMBER OF SEQ ID NOS: 3950; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 2249; LENGTH: 2267; TYPE: DNA; ORGANISM: Homo sapiens; FATURE: The Cancer of Cancer	Alignment Scores: 6.93 Length: 2267 Pred. No.: 71.00 Matches: 28 Score: 71.00 Matches: 28 Percent Similarity: 38.85% Conservative: 26 Best Local Similarity: 20.14% Mismatches: 36 Query Match: 10.50% Gaps: 4	US-10-048-196-2 (1-134) x US-09-880-107-2249 (1-2267)	Oy 20 CysAlaSerThrPro-GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLe 39	Db 1372 GGTGTCCTATGAGTGACCCTCCACACAGGTGCCTCTGAGCTGTCAGCTTCACCTGCAGGC 1313	Oy 54 yHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSe 74	Qy 74 rGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLe 94	Qy 94 uThrThrAlaAla;105 	OY 106GluvalAlaGl 109 :::::: bb :1144 ATCTTAAGAAACACTTACACTTCTTCTTACAGTTACAGTGTAAGAGATAAGTGA 1085	OY 109 nLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAlaPhe 127 :::::: ::: :::::::: Db 1084 AAAACTGACAGCGAATCTTTTGTGCAAGTCTTTTGGCAAACTGTCTTTTGTGCAAGTCTTTTGTGCAAGTCTTTTGTGCAAGTCTTTGTGCAAGTCTTTGTGCAAGTCTTTTGTGCAAGTCTTTTGTGCAAGTCTTTTGTGCAAGTCTTTGTGCAAGTCTTTTTTTT	RESULT 30 US-09-729-920-3/c
Db 597 AGCTCCACCTCCGTAACCACCATGAGCTCCTCCTTCGCCAGAACCTCCTCC 538	Oy 87 GlualaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGlu 106 	Oy 107 ValalaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126 :::::: Db 477 ATATCTCCTCCAGCACCAGCACCTTGTCCACCACCGTATCCTCC 433	Qy 127 PhellevalProThrThrThr 133 ii Db 432 ACCATGTGCACCACC 412	RESULT 28 US-09-964-824A-248/C US-09-964-824A-248/C Sequence 248, Application US/09964824A Patent V US20020102531A1 GENERAL INFORMATION: APPLICANT: Horrigan, Stephen TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu TITLE OF INVENTION: Sets FILE REFERENCE: 689290-73 FILE REFERENCE: 689290-73 FILE REFERENCE: 089290-73 FILE REFERENCE: 089290-73 FRICK PAPLICATION NUMBER: US/00/36,033 PRIOR FILING DATE: 2000-09-28 FRIOR FILING DATE: 2000-09-28	S E	Scores:	Fred. No.: 6.93 Lengun: 226/ Score: 71.00 Matches: 28 Percent Similarity: 38.85% Conservative: 26 Best Local Similarity: 20.14% Mismatches: 50 Query Match: 10.50% Indels: 35 DB: 4	US-10-048-196-2 (1-134) x US-09-964-824A-248 (1-2267)	Oy 20 CysalaSerThrPro-GluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLe 39	Qy 39 ulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGl 54 :: ::	Oy 54 yHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSe 74	Oy 74 rGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLe 94	Oy 94 uThrThralaala11eAsnProAsnAlaargThr 105 	Oy 106GluValalaG1 109 1.:::::: Db 1144 ATCTTAAGAAACACTTCTTTCTTACAGTCTTCTGGGAGTAAAGAAAAAGTGA 1085

68 32

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69. CCGGTGAGCCGCGAGAAGGCCGCATCCTCGCCGCTCTTCGCAGGTCGCCCTCGTCG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----CAACGTAGTCAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 GCTGCGACCCTCAGAGTCATTGTTGGCCTGGTGGGCAGAGCAGCAAGACGAGAATCTGTT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 AlaLysIleSerGluThrAlaCysGlyCysVal-AlaAspLysAlaProGluAlaValSe 90
                                                                                                                                                                                                                                                                                                                         33 AlaAsnLeuThrThr----SerLeuIleLysHisAlaValLysGlnThrCysGlnThr
                                                                                                                                                                                                                                                                                                                                                                                          -----AlaSerThrProGluSerAsnProLysAsnSerSer
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Mismatches:
Indels:
    ; OTHER INFORMATION: wherein any n is one of a or US-09-867-550-61
                                                                                                                                                                                                                                                                                               9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCys----
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                                                                                             Length:
Matches:
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILLING DATE: 2000-02-04
PRIOR FILLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-36
PRIOR PELLING DATE: 2000-06-03
PRIOR PELLING DATE: 2000-06-03
PRIOR PELLING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELLING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                        0.657
70.50
41.82%
26.36%
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Best Local Similarity:
Query Match:
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APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR FILING DATE: 2000-05-30
                GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000858
CURRENT APPLICATION NUMBER: US/09/729,920
CURRENT FILIG DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57383 TTCACAGACAAAGAAACTGAGACCCAGACAGGTTCAATGGCTAAGTCAAGGTTAAGCGGC 57324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIjeAsn 100
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Conservative:
Mismatches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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43.48%
22.83%
10.50%
Patent No. US20020103115A1
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Best Local Similarity:
Query Match:
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LENGTH: 455
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Patent No. US20020091244A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 ACACCTACATCACCTTCAGCGCCACCTCAAGGCCGAGGACGACGACTGAGGCCTCTGG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSED IN HELA, SIGNAL = 3.1

EXPRESSED IN HELA, SIGNAL = 4.4

EXPRESSED IN PLACENTA, SIGNAL = 4.3

EXPRESSED IN BRAIN, SIGNAL = 1.8

EXPRESSED IN LUNG, SIGNAL = 3.3

EXPRESSED IN HART, SIGNAL = 1.9

EXPRESSED IN HART, SIGNAL = 1.9

EXPRESSED IN HEART, SIGNAL = 4.2

EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
                                                     PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Matches:
Conservative:
Mismatches:
Indels:
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PCT/US01/00663
                                        APPLICATION NUMBER: PCT/US01/00662
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                 2001-01-30
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70.50
42.22%
26.67%
10.43%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-799-777-112
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LENGTH: 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SerGluThr 76
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Shah, Purvi
TITLE OF INVENTON: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
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36
21
56
22
55
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/799,777
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMÉ: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ThrLeuMetThrAlaPheThr-----
                     Hillman, Jennifer L. Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                            Baugh, Mariah
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                                                                                                                                                                                                                                                                  STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                 CORRESPONDENCE ADDRESS
Lal, Preeti
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26.67%
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                                                             Guegler,
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                             ZIP: 94304
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    APPLICANT:
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686 CCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGACC	911ACTTCTTCAGCCTCAATGTGCACAGCTGGAATTACAAGG
<pre>Qy 77 ALaCysG1yCysValaLaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96</pre>	Oy 44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet 63 ::::::
Qy 97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116 :::	Oy 64 LysLeuSerSerGluSerLysAlaLysIleSerGluThr 76
Oy 116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130 	
195-10-098-841-26 195-210-098-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 196-841-26 197-861-861-861-861-861-861-861-861-861-861	0y 97 Atablalekanerokaniakanerini :::!! ii::! bb 1127 Acaccaracaccaccaccaccaccaccaccaccaccaccac

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1998-05-07 NUMBER: 60/087106 1998-05-28 NUMBER: 60/087607 1998-06-02 1998-06-02 1998-06-02 NUMBER: 60/08759 1998-06-03 NUMBER: 60/087827 1998-06-04 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088021 1998-06-04 NUMBER: 60/088025 11998-06-04 NUMBER: 60/088025	08802 08802 08803 08803 08832 08832	08820 08821 08873 08873 08874 08882	NUMBER: 60/088858 NUMBER: 60/088861 1998-06-11 NUMBER: 60/088876 1998-06-11 NUMBER: 60/089105 1998-06-12 NUMBER: 60/089440 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089514 1998-06-17 NUMBER: 60/089538 1998-06-17 NUMBER: 60/089598 1998-06-17 NUMBER: 60/089598 1998-06-17 NUMBER: 60/089598 1998-06-17 NUMBER: 60/089598
	PRIOR AFLICATION PRIOR PRIOR PLING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR PLING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR PLING DATE: PRIOR APPLICATION PRIOR PLING DATE: PRIOR PLING DATE: PRIOR APPLICATION PRIOR PLING DATE: PRIOR FLING DATE: PRIOR APPLICATION PRIOR PLING DATE:	PRIOR APPLICATION NUMBER: 60, PRIOR FILING DATE: 1998-06-05 PRIOR PELING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60, PRIOR APPLICATION NUMBER: 60, PRIOR PLING DATE: 1998-06-05 PRIOR PLING DATE: 1998-06-05 PRIOR PLING DATE: 1998-06-10 PRIOR PELING DATE: 1998-06-10 PRIOR APPLICATION NUMBER: 60, PRIOR PELING DATE: 1998-06-10 PRIOR PELING DATE: 1998-06-10 PRIOR PLING DATE: 1998-06-10	PRIOR APPLICATION PRIOR FILING DATE: PRIOR PELING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR PILING DATE: PRIOR FILING DATE: PRIOR PELING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR PELING DATE: PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-0-17
PRIOR FILING DATE: 1998-0-6-18
PRIOR FILING DATE: 1998-0-6-18
PRIOR PRILICATION NUMBER: 60/089907
PRIOR PRILICATION NUMBER: 60/089907
PRIOR PLILING DATE: 1998-0-6-18
PRIOR APPLICATION NUMBER: 60/08948
PRIOR APPLICATION NUMBER: 60/08948
PRIOR APPLICATION NUMBER: 60/08948
PRIOR APPLICATION NUMBER: 60/08948
PRIOR PRILING DATE: 1998-0-6-19
PRIOR PRILING DATE: 1998-0-6-12
PRIOR PRILICATION NUMBER: 60/09024
PRIOR PRILING DATE: 1998-0-6-22
PRIOR PRILING DATE: 1998-0-6-23
PRIOR PRILING DATE: 1998-0-6-24
PRIOR PRILING DATE: 1998-0-6-25
PRIOR PRILING DATE: 1998-0-6-25
PRIOR PRILING DATE: 1998-0-6-25
PRIOR PRILICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-0-6-25
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PRIOR PRILICATION NUMBER: 60/09069
PRIOR PILING DATE: 1998-0-6-25
PRIOR PILING DATE: 1998-0-0-25
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1002 ACACCTACATCACCTTCAGGGGCCACTCATCAAGGCCGAGGACGACTGAGGGCCTCTGG 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LysLeuSerSerGluSer---LysAlaLysIle------SerGluThr 76
                                                                                                                                                                                                                                                              10 ThrLeuMetThrAlaPheThr--------LeuAlaSerCysAlaSerThr 23
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                                                                                                                                                                                                                                                                                                                              24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla
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                                                                                                                                  Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                    Length:
                                                                                                                                                                                                 Gaps:
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 66/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 66/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Goddard, Audrey
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                                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                 Alignment Scores
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TITLE OF INVENTION: Secreted and Transmembers Polypeptides and Nucleif COURREW TAPLICATION WANDER: 19730-173.

PRICE REFERENCE: P2330-166.

PRICE REPLICATION WANDER: 19730-173.

PRICE REPLICATION WANDER: 05/043787

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PRICE REPLICATION WANDER: 05/043787

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PRICE REPLICATION WANDER: 1997-11.12

PRICE REPLICATION WANDER: 1997-11.13

PRICE REPLICATION WANDER: 1997-11.13

PRICE RELING DATE: 1997-11.13

PRICE RELING DATE: 1997-11.13

PRICE REPLICATION WANDER: 05/04510

PRICE RELING DATE: 1997-11.13

PRICE REPLICATION WANDER: 1007-11.13

PRICE RELING DATE: 1997-11.13

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A APPLICATION NUMBER: 60/089538
A FILING DATE: 1998-06-17
A APPLICATION NUMBER: 60/089598
A FILING DATE: 1998-06-17
A APPLICATION NUMBER: 60/089599
A FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
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                              APPLICATION DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
APPLICATION NUMBER: 60/089410
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LING DATE: 1998-06-18
PPLICATION NUMBER: 60/089947
LING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-24
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TILING DATE: 1998-06-19
PPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-17
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NG DATE: 1998-06-19
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1002 ACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACTGAGGGCCTCTGG 1061 942 GCGTCTGGGTGCGGCTCTTCAAGCGCCAGGGGAAGGCCCATCTACAGCAACGACTTCG 1001 97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116 726 ACCITGATGGGTGCTTTGACATGCCGACCGGCCAGTTTGCTGCTCCCTGCGTGGCATCT 785 882 CCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACC 941 :::::|||||| :::||||||| | :::|||| | :::|||| | ::: 77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96 44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet 63 10 ThrLeuMetThrAlaPheThr-------LeuAlaSerCysAlaSerThr 24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla ---SerGluThr 116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130 LysLeuSerSerGluSer---LysAlaLysIle------Conservative: Mismatches: Indels: US-10-048-196-2 (1-134) x US-09-989-293A-46 (1-3089) Matches: R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090862
R APPLICATION NUMBER: 60/090863
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R APPLICATION NUMBER: 60/091360
R APPLICATION NUMBER: 60/091360 Sequence 46, Application US/09989735 Publication No. US20020193299A1 GENERAL INFORMATION: APPLICATION NUMBER: 60/091626 FILLING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILLING DATE: 1998-07-02 ICATION NUMBER: 60/090695 NG DATE: 1998-06-25 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 13.3 70.50 42.228 26.678 10.438 Percent Similarity: Best Local Similarity: Query Match: US-09-989-735-46 Alignment Scores: .. 9 PRIOR
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APPLICANT: Ashkenazi,Avi a APPLICANT: Baker,Kevin P

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R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
R FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089598
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PPLICATION NUMBER: 60/089599
TLING DATE: 1998-06-17
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-00
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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LOR FILING DATE: 1997-11-12
LIOR APPLICATION NUMBER: 60/065311
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LIOR APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/075945
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FILING DATE: 1998-06-05
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Williams, P. Mickey
Wood, William I.
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tewart, Timothy A
umas, Daniel
                                                           errara, Napoleone
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Goddard, Audrey
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                                                                                                     Gerber, Hanspeter
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                                                                                                                                                                    Godowski, Paul
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1002 ACACCTACATCACCTTCAGGGCCACCTCCATCAAGGCCGAGGACGACTGAGGCCTCTGG 1061
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CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250
    882 CCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGGTGGACCTGGCCTACGGGGACC 941
                                                                                                                                    97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116
                                                           77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96
                                                                                                                                                                                                                                                      1062 GCCACCCTCCCGGCTGGAGCTCAGGTGCTGGTCCCGTCCCC 1104
                                                                                                                                                                                                                 116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130
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R APPLICATION NUMBER: 60/065186

R RELING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

R R PILING DATE: 1997-11-13

R APPLICATION NUMBER: 60/066770

R APPLICATION NUMBER: 60/066770

R R APPLICATION NUMBER: 60/06571

R R APPLICATION NUMBER: 60/05945

R R PILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/08332
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/09990444 Publication No. US20020193300A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/08/106
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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Stewart, Timothy A.
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Watanabe, Colin K
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Goddard, Audrey
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Botstein, David
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Stewart, Truc
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APPLICATION NUMBER: 60/090535
                                                                                             APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
                                                       APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-04
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APPLICATION UNMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 PLICATION NUMBER: 60/089599 009680/09 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 60/087759 LICATION NUMBER: 60/087827 ING DATE: 1998-06-03 60/088033 60/088734 60/088824 PLICATION NUMBER: 60/088861 APPLICATION NUMBER: 60/088021 LING DATE: 1998-06-10 PLICATION NUMBER: 60/0 LING DATE: 1998-06-11 PLICATION NUMBER: 60/ 1998-06-10 LING DATE: 1998-06-05 LING DATE: 1998-06-05 LING DATE: 1998-06-10 1998-06-10 LING DATE: 1998-06-16 LING DATE: 1998-06-04 1998-06-04 1998-06-04 1998-06-09 1998-06-12 1998-06-17 1998-06-17 1998-06-17 1998-06-0 LING DATE: 1998-06-1 1998-06-1 LING DATE: 1998-06-ING DATE: 1998-06 LICATION NUMBER: ING DATE: 1998-06 LICATION NUMBER: APPLICATION NUMBER: PLICATION NUMBER: APPLICATION NUMBER: PLICATION NUMBER: APPLICATION NUMBER: PLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: LING DATE: FILING DATE: FILING DATE: LING DATE: LING DATE: LING DATE: PRIOR
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R PAPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 FILLING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 089947 APPLICATION NUMBER: 60/090355 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 60/090435 APPLICATION NUMBER: 60/090445 60/090472 60/090535 80/090678 APPLICATION NUMBER: 60/090690 60/090862 60/091544 APPLICATION NUMBER: 60/091519 60/091633 60/091982 60/092182 60/090444 60/090557 60/090694 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/C FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/C FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/0 1998-06-22 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ 1998-06-25 1998-06-25 1998-06-26 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/ 1998-07-02 FILING DATE: 1998-07-09 1998-06-23 1998-06-24 1998-07-02 1998-06-24 1998-07-01 998-07-02 998-06-24 LING DATE: 1998-06-2 1998-06-2 TLING DATE: 1998-06-2 FILING DATE: 1998-07 APPLICATION NUMBER: FILING DATE: 1998-07 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: TILING DATE: PRIOR PRIOR

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                                                                                                                          24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43
                                                                                                                                                                                                                                        44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet 63
                                                                                                                                                                                                                                                                                              -----SerGluThr 76
                                                                                                                                                                                                                                                                                                                                                    77 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96
                                                                                                                                                                                                ----ACTTCTTCAGCCTCAATGTGCACAGCTGGAATTACAAGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 uLysProCysMetLeuGluThrValAsnAlaPhelleValPro 130
Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              US-10-048-196-2 (1-134) x US-09-990-444-46 (1-3089)
                                                                       Gaps:
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Sequence 46, Application US/09989730

Publication No. US20020197674A1

GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Botstein, David
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FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 'ILING DATE: 1998-04-28 PPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 ILING DATE: 1998-06-04 PPLICATION NUMBER: 60/088025 LICATION NUMBER: 60/088030 ILING DATE: 1998-06-04 PPLICATION NUMBER: 60/088167 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 PPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/065311 APPLICATION NUMBER: 60/075945 PPLICATION NUMBER: 60/087609 APPLICATION NUMBER: 60/087759 PPLICATION NUMBER: 60/087827 ILING DATE: 1998-06-03 PPLICATION NUMBER: 60/088021 LICATION NUMBER: 60/088026 PPLICATION NUMBER: 60/088028 PPLICATION NUMBER: 60/088029 PPLICATION NUMBER: 60/088033 PPLICATION NUMBER: 60/088326 PPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088810 PPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 ILING DATE: 1998-06-10 LING DATE: 1998-03-20 ILING DATE: 1998-06-05 ILING DATE: 1998-06-05 LING DATE: 1998-06-09 ILING DATE: 1998-06-10 998-06-02 LING DATE: 1998-06-02 ILING DATE: 1998-06-04 LING DATE: 1998-06-04 1998-06-04 01-90-866 'ILING DATE: 1998-06-10 998-06-10 998-06-04 998-06-04 0-90-866 998-06-1 998-06-1 PPLICATION NUMBER: LING DATE: 1 LING DATE: LING DATE: LING DATE: LING DATE: ILING DATE: LING DATE:

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FILING DATE: 1998-06-26
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ICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090678
                             PLICATION NUMBER: 60/089514
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RAPLICATION NUMBER: 60/091544

RAPLICATION NUMBER: 60/091519

RAPLICATION NUMBER: 60/091519

RELLING DATE: 1998-07-02

RAPLICATION NUMBER: 60/091626

RELLING DATE: 1998-07-02

RAPLICATION NUMBER: 60/09163

RELLING DATE: 1998-07-02

RAPLICATION NUMBER: 60/09198

RELLING DATE: 1998-07-07

RAPLICATION NUMBER: 60/091982

RELLING DATE: 1998-07-07

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RELLING DATE: 1998-07-07

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RAPLICATION NUMBER: 60/09182
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                                                        APPLICATION NUMBER: 60/091478
                    60/091360
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Fong, Sherman
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                      APPLICATION NUMBER:
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APPLICATION NUMBER: 60/08824
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Grimaldi, J.Christopher
                                                                                                         Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                                                                                Roy, Margaret Ann
Stewart, Timothy A
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Page 28

Length:
Matches:
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Mismatches:
Indels:
Gaps: 13.3 70.50 42.22% 26.67% 10.43% Percent Similarity: Best Local Similarity: Query Match: Pred. No.:

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1998-07-07

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US-10-048-196-2 (1-134) x US-09-990-436-46 (1-3089)

882 CCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACC 941 ---AGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCATCCTGTACGCGCAGC 881 ----LeuAlaSerCysAlaSerThr 23 44 ValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet 63 64 LysLeuSerSerGluSer---LysAlaLysIle------SerGluThr 76 AlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThr 96 24 ProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 10 ThrLeuMetThrAlaPheThr----786 825 17 g g ò ð g ò ð g δ

1002 ACACCTACATCACCTTCAGCGCCCACCTCAACAAGCCCGAGGACGACGACGACGACGACTCTGG 1061 97 AlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIle-ValArgHisSerLe 116 QΩ

116 uLysProCysMetLeuGluThrValAsnAlaPheIleValPro 130

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1062 GCCACCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCC 1104

Search completed: May 5, 2003, 23:56:37 Job time : 128 secs

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2047.354 Million cell updates/sec
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Run on:

32308132 Total number of hits satisfying chosen parameters: 16154066 seqs, 8097743376 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Over Outer Date							
1 98.5 14.6 476 17 A0886059 AQ886059 2 95 14.1 1813 14 B0835107 B0835107 3 94.5 14.0 769 14 B08004254 B08004254 6 94.5 14.0 769 14 B08004254 B08007264 9 13.9 14.0 784 14 B08007264 B08007264 9 13.9 10.0 10 MAISA646 MAISA646 9 13.6 679 17 AA258694 AA358694 10 91 13.5 610 14 B0600421 11 90 13.3 787 14 B0600429 11 90 13.3 787 14 B0600429 12 90 13.3 787 14 B0600429 13 90 13.3 787 14 B0600429 14 B0204046 B0804264 AA358664 <t< th=""><th>Result</th><th>cor</th><th>Query Match</th><th>Length</th><th>Ω</th><th>Ω</th><th>scripti</th></t<>	Result	cor	Query Match	Length	Ω	Ω	scripti
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5 87 12 9 720 14 B0246266		87		720		024626	3266 TAR150

AQ886059 476 bp DNA linear GSS 09-NOV-1999 HS_5530_B2_C07_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9298 Col=14 Row=F, DNA sequence. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 476)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and ÄQ886059 AQ886059.1 GI:6317526 human. RESULT 1 AQ886059/c LOCUS DEFINITION ORGANISM AUTHORS ACCESSION REFERENCE KEYWORDS SOURCE VERSION

ALIGNMENTS

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preparations and DNA sequencing were performed in the OD
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                                                        High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 516-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 9298 row: F column: 14
Seq priner: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector EcoRI sites" 3 others
              A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TTACAGAGCCCCTCTANAGCCAAGTGGGTCCCCAACTTCTGCTCTATCAGAGGAGACAGT 183
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380 acacatggcatgggtcagagtggaatatgcaggaagtcatgcattgacattcctcatctg 321
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                  scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref="traxon:9606"
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Location/Qualifiers
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'Triticae; Triticum.

Triticae; Triticum.

I (bases 1 to 813)

RS Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin, K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.

The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library

Unpublished (2002)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Arac, Western Regional Research Center 800

Buchanan Street, Albany, CA 94710, USA

Tel: 5105595718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOORI: Plants were grown under six following different environmental regimes in greenhouse, Environment 1)
240c/Inoc day/Anight, well-watered, with post-anthesis fertilizer, Environment 2) 240c/Inoc day/Anight, well-watered, without post-anthesis fertilizer, Environment 2) 370c/Inoc day/Anight, well-watered, without post-anthesis fertilizer, Environment 4) 370c/Inoc day/Anight, well-watered, without post-anthesis fertilizer, Environment 5) 370c/Inoc day/Anight plus drought, without post-anthesis fertilizer, Environment 6) 370c/Inoc day/Anight plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A conn at USDA-ARS, Hibrary was made using poly (A) RNA, and the cDNA clones were in vivo excised to give plauescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside Fenton) at the
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WHE3589_D08_H152S Wheat developing grains cDNA library Triticum
aestivum cDNA clone WHE3589_D08_H15, mRNA sequence.
BQ839107
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Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, Pooideae
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140 GGGGAATTCCTTTTTACACTÀGTAACCCACCAAAGAAGGGAAIGTTCATTITACACCCTT 81
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/lab_host="E. coli SOLR"
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/db_xref="taxon:4565"
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1. .813
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source 1.		24 Fee			L L	Ur Pl Ar Ar Coliny 234 a	IN Inent Scores:	Fred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	US-10-048-196-2 (1-134)	139	199	241	Db 301 TACTTACCAGCT	Db 361 GCAGTGCCAGGC Qy 90 SerLeuThrGlu Db 406 TCAACAAAAA
Anderson lab (others)." F 276 a 258 c 126 g 153 t	Alignment Scores: 0.699 Length: 813 Score: 95.00 Matches: 36 Percent Similarity: 41.738 Conservative: 22 Best Local Similarity: 25.908 Mismatches: 47 Query Match: 14.058 Indels: 6	(1-134) x BQB39107 (1-813) *AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer	2/ ASINTOLYSASIOSTSEATABASILEUTITINES TEGILEBYSHISAIAVALLYSCIN 46 1	65 LeuserSerGluserLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLys 84	CCCGGAGTIGTCAAGTCCAAGTCAATGTCGTTCATGTTATTCTGCA	ThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluVal 107	AlaGlnLyslleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126 :::		BQ804850.1 GI:22029059 EST.		: Triticeae; Triticum. I (bases 1 to 709) Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin X., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,		Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 510595773	Fax: 51U5595818 Email: oandersn@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer. Location/Qualifiers
BASE COUNT ORIGIN	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	-10-048- 7 336	OY 2/ Db 396 OY 47 Db 438	Oy 65 Db 498	ιΛ	Oy 92 Db 600	Qy 108 Db 660	RESULT 3 BQ804850 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE · AUTHORS	TITLE	COMMENT	FEATURES

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/clone_ib="Wheat developing grains cDNA library"
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/dev_stage="3.44 days post anthesis seed"
/lab_host="E. coli SOLR"
/lab_host="E. coli Solr Solr"
/lab_host="E. coli Sol
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Matches:
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                                     /db_xref="taxon:4565"
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cultivar="Butte 86"
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BQ807264 Tinear 1 EST 31-JUL-2002 WHE3588_G02_M04ZS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3588_G02_M04, mRNA sequence.
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Rejonal Research Center
800 Buchanan Street, Albany, CA 94710, USA
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Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
Wilson, C. and Woo, J.
Wilson, C. and Moo, J.
Wilson, C. and Woo, J.
Wilson, C. and Woo, J.
Wilson, C. Seveloping grains cDNA library
Unpublished (2002)
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Conservative:
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     164
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Fax: 5105595818
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BQ807264
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/cultivar="Butte 86"
/dutivar="Butte 86"
/dutivar="Butte 86"
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/dutivar="Butte 86"
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/clone="Wheat developing grains cDNA library"
/tissue_type="and adveloping grains"
/dev_stage="3-44 days post anthesis seed"
/dab_host="E. coli SoLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
24oc/Inco day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24oc/Inco day/night, well-watered, without post-anthesis fertilizer,
Environment 3) 37oc/Inco day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 37oc/Inco day/night bus drought, with
post-anthesis fertilizer, Environment 6) 37oc/Inco
day/night plus drought, without post-anthesis fertilizer,
Environment 5) 37oc/Inco day/night plus drought, without post-anthesis fertilizer,
Environment 6) 37oc/Inco day/night plus drought, without post-anthesis fertilizer,
Environment 1 2, 37oc/Inco day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 35, 40, 40, 44 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 20, 24, 28, 30 DPA and total RNA was prepared by S.
Altenbach and K. Cronin at USDA-NRS, Albany CDNA
library was made using poly (Ah RNA, and the CDNA
library was made using poly (Ah RNA, and the CDNA CALIGORNA)
library was made using po
                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.

1 (bases 1 to 769)
Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin
Ak., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J.,
Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                 EST 31-JUL-2002
                                                                                                                                                                                           BQ804254 linear EST 31-JUL-;
WHE3552_CO6_E12ZS Wheat developing grains cDNA library Triticum
aestivum cDNA clone WHE3552_CO6_E12; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer.

Location/Qualifiers
                          110 LysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126
                                                       466 ACAATA-----TCCATTAGGCCAGGCTCCTTCCGGCCATCTAGCA 507
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                                                                                                                                                                                                                                                                                                        BQ804254.1 GI:22028238
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Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                        EST.
bread wheat
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1080 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6459878 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5581015
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
Tissue Procure
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1080) NHH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Nih_mu-_v.,
/tissue__type="retinoblastoma"
/lab_bost="DH10B (phage-resistant)"
/note="noran: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Site_2: SalI; Cloned unidirectionally. Primer: Oligo (Site_2: SalI; Cloned unidirectionally. Primer: Oligo (Site_2: SalI; Cloned unidirectionally.)
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110 LysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsnAla 126
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Best Local Similarity:
Query Match:
                                                         697 ACAATA----
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                                                                                                                                                                                                              /lab_host="E. coli SOLR"
//note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI: Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
24oC/17oC day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24oC/17oC day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 37oC/17oC day/night, well-watered, without post-anthesis fertilizer,
Environment 3) 37oC/17oC day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 37oC/17oC day/night plus drought, with
post-anthesis fertilizer, Environment 4) 37oC/17oC
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 37oC/17oC day/night plus drought, without post-anthesis fertilizer,
day/night plus drought, without post-anthesis fertilizer,
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.
Altenbach and R. Cronin at USDA-ARS, Albany, CA.
Ilbrary was made using poly (A) RNA, and the cona clones
were in vivo excised to give pBluescript SK(-) phagemids
in the TJ Close lab (Chin, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (others)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 GTATTCGCAACCACAAGAACCAATTTCACAGCAGCAGCAACAACAACAACAACAACAACA
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532 TACTTACCAGCTATTGCAATTGTGTGTGTGTGAGCACCTATGGCAGATCCCTGAGCAGTC 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer
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                                                                                  /clone="WHE3588_G02_M04"
/clone_lb="Wheat developing grains cDNA library"
/tissue_type="Whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
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Matches:
Conservative:
Mismatches:
Indels:
   organism="Triticum aestivum"
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AW504179 427 bp mRNA linear EST 02-MAR-2000 UI-HF-BNU-ale-f-08-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079431 5', mRNA sequence.
AW504179.1 GI:7141846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 427)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collegtion (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-rémail.nih.gov

Eco RI site shown at the bequinning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D. Ph.D.

CDNA Library Preparation: M.B. Soares Lab.

CDNA Library Arrayed by: M.B. Soares Lab.

DNA Sequencing by: M.B. Soares Lab.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbry/image.image.html

Seq primer: MI3 Porward.
    282.ACTCCAGGCCAAGCTC-----CACCTCGCCTGGAAATGGTTATCTCCTGAAATCGGCA 335
                                                                                                                                                                           336 GCAGTGACAGTGGCCGGTTCAGCGTCAGGGCCTGTGGCTGTGCCCAGCTCTGACATGTCT
                                                                                                                                     -----ValAlaAspLys----
                                                                                                                                                                                                                                        erGluSerLysAlaLysIleSerGluThrAlaCysGlyCys
                                                                                                                                                                                                                  86 roGluAlaValSerLeuThrGluLeuThrThrAlaAla 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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13.688
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TITLE
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AW504179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gcr.irken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                           09-JAN-2002
                                                                                                                                                                                                                                                                                      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-023L05.TJ.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
:: ::: ::: 491 CCAGCAGAACAGCTCAAACGCAACAAGGCCCAAACTCATGCAG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 CCTGCAAGCTCACCAGCAAACTGTGCTGTCCAGTCCCTCAAACTCCAAACCAAGCCCAC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 ProLysAsnSerSerAlaAsn-LeuThrThrSerLeuIleLysHisAlaValLysGlnTh 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 rCysGlnThrGlnLeuThrGlyHis-GlnTyrTrpLysIleAlaAlaMetLysLeuSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer---Asn
                                                      -----ThralaalaIleAsnProAsnAlaArgThrGluValAla 108
                                                                                AG158466 679 bp DNA 11near GSS 09 Pan troglodytes DNA, clone: RP43-023L05.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
231 c 137 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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37
113
38
26
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Matches:
Conservative:
Mismatches:
Indels:

    .679
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
    /clone="RP43-023L05.TJ"

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1. 679
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: Ecori
: Ecori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of clone tracking errors
PRIMERS
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AG158466.1 GI:16688144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing: TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 679)
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43.868
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R.Site 2
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AUTHORS
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/cell_type="germinal center B cells"
/cell_line="MGCB5"
/lab_host="bHi0B (LTI)"
/note="Vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5.4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Louis M. Staudt, Ph.D. and M. Bento Soares, Ph.D. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSer---Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TCTACTGTCTCCACGGCCACTAGTTTACCTTTGGCAGCACTCCGGCAGCTCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                 427
29
12
29
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Mismatches:
Indels:
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Matches:
                                              /clone_lib="NIH_MGC_50"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
/db_xref="taxon:9606"
/clone="IMAGE:3079431"
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VERSION
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymorlectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                 GSS 02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 679)

Dunn,D., Aoyad,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                  1M0101817F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0101817 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                      273 ACTCCAGGCCAAGCTC----CACCTCGGCCTGGAAATGGTTATCTCCTGAATCCGGCA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                               67
47
ProLysAsnSerSerAlaAsn-LeuThrThrSerLeuIleLysHisAlaValLysGlnTh
                                                                           47 rCysGlnThrGlnLeuThrGlyHis-GlnTyrTrpLysIleAlaAlaMetLysLeuSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/dboe="UGCIM0101B17"
/clone="UGCIM0101B17"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                               erGluSerLysAlaLysIleSerGluThrAlaCysGlyCys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 10000 Std Error:
Plate: 0101 row: B column: 17
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 679.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        AZ358694.1 GI:10472394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801,585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
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AJ452083 AJ52083 rikenl Gallus gallus cDNA clone 2m15r1, mRNA sequence. AJ452083
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1 (bases 1 to 811)

Buerstedde,J.M.

Gallus gallus bursal lymphocyte EST

Onpublished (2002)

Contact: Buerstedde JM

Cellular Immunology
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1. 811
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and selected for ampicillin resistance." 147\ ^{\circ} 102\ g 244\ t
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222
52
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Mismatches:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum
; (bases 1 to 630)
Clarke, B., Lambrecht, M. and Rhee, S.
Assessing the utility of Arabidopsis genomic information for Interpreting wheat EST sequences
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ606191 630 bp mRNA linear EST 25-JUN-2002 BRY_2034 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence.
BQ606191 GI:21555417
                                                                                                                                                                                                                                                                                                          368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 ThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSer 115
                                                                                                                                                                                                                                                                                                                                                                         249 CCGAGCAAAATGGCAACACTGATGGCAAAAATGGCCAGGAAGATGACAACACCGATGGCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 AAGGTGAGAACACTGACAAGCAGCCACCCAGCAAGGCAGCAGCAACTCACAAGATAACA 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 LysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
                                                                                                                                                                                                                                                                                        8 ThralaThrLeuMetThralaPheThrLeuAlaSerCysAlaSerThrProGluSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                  28 ProLysAsnSerSerAla----------AsnLeuThrThrSerLeuIle
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                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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/clone="2m15r1"
/clone_lib="riken!"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
a 229 c 195 g 66 t
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MHE3586_A07_B142S Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3586_A07_B14, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 787)
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                                                                  /db_xref="taxon:4565"
/db_xref="taxon:4565"
/clone_lib="wheat EST endosperm library"
/tissue_type="endosperm"
/dex_stage="developing endosperm tissue 8,
(days_post_anthesis)"
/note="vector: Bluescript_II SK(-)"
                                                                                                                                                              Bluescript II SK(-)"
00 g 117 t 5 others
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20
20
84
88
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Mismatches:
Indels:
                                     /organism="Triticum aestivum"
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Matches:
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Location/Qualifiers
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                                                      /cultivar="Wyuna"
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-CAG 485

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (base; Triticum.

1 (bases 1 to 812)
Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin,K., Crossan,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECORI; plants were grown under six following different environmental regimes in greenhouse, Environment 1) 420/170c day/night, well-watered, with post-anthesis fertilizer, Environment 2) 240C/170c day/night, well-watered, without post-anthesis fertilizer, Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170c day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 6) 370C/170C
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The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ804628 812 bp mRNA linear EST 31-JUL-2
WHE3555_H07_014ZS Wheat developing grains cDNA library Triticum
aestivum cDNA clone WHE3555_H07_014, mRNA sequence.
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/lab_host="E. coll SOLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                                                                                               |||||||:::::
| CGAGCAGTGCGGGTGCCAAGCCATCCACAATGTTGTTCATGTTATTCTGCATCAACA 656
                                                                                                                                                                                                                                                                                                                                                                                                                           92 ---ThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLys 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 AAGTACTTACCAGCTGGTGCAACAATTGTGTTGTCAGCAGCTGTGGCAGAT-----CCC 596
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                                                                47 ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSer
                                                                                                                                                                                   67 SerGluSerLysAlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaPro
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            444 GATCCTTCAACAATTTTGCAACAACAACTGATTCCATG-
                                                                                                                                                                                                                                                                                                         87 GluAlaValSerLeu-------
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Fax: 5105595818
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//Librare="Wherest developing grains clone_lib="Wheat developing grains clone_lib="Wheat developing grains clone_lib-"Wheat days post anthesis seed"
//Lab_host="E. coli SOLR"
//Librarest days more grown under six following different environmental regimes in greenhouse, Environment 1)
240c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 2) 240c/170c day/night, well-watered, without post-anthesis fertilizer, Environment 3) 370c/170c day/night, well-watered, without post-anthesis fertilizer, Environment 4) 370c/170c day/night plus drought. without post-anthesis fertilizer, day/night plus drought, without post-anthesis day 1 day 3, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.
Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cobna library was made using poly (A) RNA, and the CDNA clones
                                                                                                                                                                             Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preparations and DNA sequencing were performed in the OD
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in the TJ Close lab (Chin, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library
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Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
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/cultivar="Butte 86"
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        BJ233642 Colhara unpublished cDNA linear EST 05-APR-2002 BJ233642 Y. Ogihara unpublished cDNA library, Wh_e Triticum aestivum cDNA clone whe6jl7 5'', mRNA sequence.
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1 (bases 1 to 610)
Ogihara, Y. and Murai, K.
 without post-anthesis fertilizer
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/clone_lib_gray.
/tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/dev_stage="Feekes' scale 11.2"
/note="Wedror: Lambda Uni_ZAP XR, excised phagemid;
/notes, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yatta, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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/db_xref="taxon:4565"
/clone="whe6j17"
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                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.97
89.50
37.84%
24.32%
13.24%
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Best Local Similarity:
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CysMetLeuGluThrValAsnAla 126

119

101

81

74

Tue May

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/tissua_type="developing seeds"
/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcWv-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 15 days post-anthesis"
204 c 115 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae, Triticeae; Triticeae; Triticum.
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ246193 671 bp mRNA linear EST 03-MAY-2002 TaE15015A03R TaE15 Triticum aestivum cDNA clone TaE15015A03R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tal: (204) 983-2340

Fax: (204) 983-4604

Fax: (204) 983-4604

Email: scloutier@em.agr.ca

primer were from the 5' end (same with forward primer and 3' end).

Average insert size is >1.4 kb

Plate: 015 row: A column: 03

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGTCCTTCCAACAGCCTCTGCAAAAA------TCCATTAGGCCAGGGCTCCTT 379
                                                                                                                                                                    284 ------TATTCTGCATCAACAAAAACAACAACAACAACAACAACAACGAGCA 328
                                                                                                                                                                                                                                                                                                               164 AAGATCACAAGTTTTGCAACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTGTTGTCAGCA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                         224 CCTATGGCAGATCCCTGAGCAGTCGCAGTGTCAGGCCATCCAAAATGTTGTTCATGCTAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AsnAlaArgThrGluValAlaGlnLySIleValArgHisSerLeuLysProCysMetLeu 121
                                                              62 ACAACAACAACAACAACAAAAGCAAATCCTTCAACAATTTTGCAACAACAACTGATTCC 121
------SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSer 38
                                                                                                                         39 LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp 58
                                                                                                                                                                                                                                                   59 Lysile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer---
                                                                                                                                                                                                                                                                                                                                                                       -----GluThrAlaCysGlyCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 AlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnPro
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/db_xref="taxon:4565"
/clone="TaE15015A03R"
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BQ246193.1 (
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TITLE
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COMMENT
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BQ246193
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Site_1: ECORI; Site_2: XhoI; Spikes at 5, 10, 15 and 20
days after anthesis were heat stressed under two
conditions at Texas Tech University (D. Zhang in HT Nguyrn
lab): (1) at 38 C for 4 hours and (2) 5 days of cyclic
treatment of 38 C for 4 hours. Total RNA and poly(A) RNA
were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton, Malatrasi) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                    BF429171 646 bp mRNA linear EST 29-NOV-2000 WHE1709_C12_E232S Wheat heat stressed spike cDNA library Triticum aestivum cDNA clone WHE1709_C12_E23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viriliplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Triticae; Triticae.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/cultiva="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1709_C12_E23"
/clone="WHE1709_C12_E23"
/tlone="Wheat heat stressed spike cDNA library"
/tissue_type="Whole spike"
/dev_stage="Spikes at 5, 10, 15 and 20 days after
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Mismatches:
Indels:
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Matches:
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GGGCTTCTTCCAACCATCTCAGCA 610
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BF429171.1 GI:11441095
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89.50
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VERSION
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COMMENT
                          587
                                                                                        RESULT 15
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us-10-048-196-2.rst

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/clone="TagE15030801R"
/clone=lib="TagE15030801R"
/tissue_type="developing seeds"
/tissue_type="developing seeds"
/tab_host="E. coli DH10B"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: Not1; Site_2: Mlu1; mRNA obtained from wheat seeds
of cultivar Gleniea 15 days post-anthesis"
a 223 c 107 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ246348 754 bp mRNA linear EST 03-NAY-2002 TaE15012H10R TaE15 Triticum aestivum cDNA clone TaE15012H10R, mRNA sequence.
BQ246348.1 GI:20442224
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
; Triticeae; Triticum.
1 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 AlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 -----CAGGGATGTTGTATTGCAACAACATAGCGCATGGAAGCTCACAAGT
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
                                                                                                                                                                                                                                                                                                                                                           7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAla-----
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Mismatches:
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Matches:
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13.24%
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Best Local Similarity:
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SOURCE
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BQ246348
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TITLE
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-404
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 030 row: B column: 01
Seq primer: M13 Reverse.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae,
, Triticeae; Triticum.
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TaE15030B01R TaE15 Triticum aestivum cDNA clone TaE15030B01R, mRNA
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                                                                                                                                                                                                             23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                                                                                                                                                            99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro
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                                                                                                                                              7 ValThralaThrLeuMetThralaPheThrLeuAlaSerCysAla---
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                                   Conservative:
Mismatches:
Indels:
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     Length:
Matches:
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                                                                                                              US-10-048-196-2 (1-134) x BQ246193 (1-671)
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BQ245146.1 GI:20441022
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13.24%
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Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-24604
Email: scloutiereem.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Table"
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/tissue_type="developing seeds"
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Site_1: NoTI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
101 g 127 t
вимагуота; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum
                                                                                                                                                                                                                                             was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >1.4 kb Plate: 019 row: D column: 12 Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 HisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle---
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Mismatches:
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Matches:
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1 (bases 1 to 677)
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/dev_stage="15 days after anthesis"
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/lab_host="Te. coli DH10B"
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Site_1: NoII; Site_2: MHUI; mRNA obtained from wheat seeds of cultivar Glenlea 15.days post-anthesis"
203 c 129 g 169 t
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                                                                                was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >1.4 kb Plate: 012 row: H column: 10 Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 TACTTACCAGCTGTTGCAAGAATTGTGTTGTCAGCACCTATGGCAGATCCCTGAGAAGTT 333
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TTel: (204) 983-2340
Farx: (204) 983-4604
Email: scloutier@em.agr.ca
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Matches:
Conservative:
Mismatches:
Indels:
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Wheat functional genomics - Gleniea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2346
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcw/vsPokT6.0 (Invitrogen Technologies);
Site_1: NotI: Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
235 c 111 g 134 t
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TaE15010E09R TaE15 Triticum aestivum cDNA clone TaE15010E09R, mRNA
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       --GluThrAlaCysGlyCysValAlaAspLys
                                                                    381 GATCCCTGAGCAGTCGCAGTGCCAGGCCATCCACAAAGTTGTTCATGCTAT-----
                                                                                                                                         85 AlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsnAlaArg
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/db_xref-"taxon:4565"
/clone-"TaE15010E09R"
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BQ246454.1 GI:20442330
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/organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE15008E10R"
/clone="TaE15008E10R"
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/note="Vector: pcMV-SPORT6.0 (Invitrogen Technologies);
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Wheat functional genomics - Glenlea developing seeds cDNA libraries
Unpublished (2002)
Contact: Dr. Sylvia Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd. Winnipeg, MB, Canada R3T 2M9
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Fax: (204) 983-4604
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, Pooldeae
; Triticeae, Triticum.
                                                                                                                                                                  BQ246558 13-MAY-2002 694 bp mRNA linear EST 03-MAY-2002 Tab15008E10R Tab15 Triticum aestivum cDNA clone Tab15008E10R, mRNA
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fertilizer, Environment 2) 24oC/17oC day/night, well-watered, without post-anthesis fertilizer, Environment 3) 37oC/17oC day/night, well-watered, with post-anthesis fertilizer. Environment 4) 37oC/17oC day/night, well-watered, without post-anthesis fertilizer, Environment 5) 37oC/17oC day/night plus drought, with post-anthesis fertilizer, Environment 6) 37oC/17oC day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 pps Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPR Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPR environment 6 environment 6 environment 6 environment 6 environment 6 environme	Alignment Scores: 4.12 Length: 792 Pred. No.: 88.50 Matches: 36 Score: 88.50 Matches: 36 Percent Similarity: 37.84% Conservative: 20 Best Local Similarity: 34.32% Indels: 51 Query Match: 13.09% Indels: 41 DB: 14 Gaps: 7 US-10-048-196-2 (1-134) x BQ839009 (1-792)	AlaThrLeuMetThrAlaP	61	99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 711 GTTGAGCCAGGTCTCTTCCAGCAGCTCAGCAATATCCATCAGGCCA 119 CysWetLeuGluThrValAsnAla 126 119 CysWetLeuGluThrCaAcCATCTCAGCA 785 1262346 123 GGCTTCTTTCAACCATCTCAGCA 785 1262346 127 GGCTTCTTTCAACCATCTCAGCA 785 1262346 128 GGCTTCTTTCAACCATCTCAGCA 785 129 CGCTTCTTTCAACCATCTCAGCA 785 129 CGCTTCTTTCAACCATCTCAGCA 785 120 CGCTTCTTTCAACCATCTCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACATCAGCAACAACAACAACAACAACAACAACAACAACAACAAC
Qy22 SerThrProGluSerAsnProLysasnSerSerAlaAsnLeuThrThrSerLeuIleLys 41Db321 ACAACAACAACAAATCTTCAACAATTTGCAACAACTTCCATGCTTCCATGCTTCCATGCTTCCATGCTTCCATGCTTCCATGCTTTCCATGCTTTCCATGCTTTTTGCAACAACTTTTTTTT	2 2 ON	SOURCE SOURCE Dread wheat. ORGANISM Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum. REFERENCE 1 (bases 1 to 792) AUTHORS Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Milson,C. and Woo,J. TITLE The structure and function of the expressed portion of the wheat genomes - Developing grains cDMA library.	JOURNAL Unpublished (2002) COMMENT Contact: Oll Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 510559578 Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer:	rce

us-10-048-196-2.rst

Db 252 AGTTTTGCAACAAGTACTTACCAGCTGTTACAAGAATTGTGTTGTCAGCACCTATGGCA 311 Qy 75		FEATURES Location/Qualifiers Location/Qualifiers 1. 708 / Organism="Triticum aestivum" / Orlone="Triticum a
ACCESSION ACCESSION BG262346 BG262346.1 GI:12863468 KEYWORDS BC26346.1 GI:12863468 KEYWORDS BC362346.1 GI:12863468 EST CORGANISM FILICUM aestivum COGANISM FILICUM aestivum COGANISM FILICOM FILIN FILICOM FILICOM FILICOM FILICOM FILICOM FILICOM FILICOM	Seq primer: Stratuagene SK primer. Location/Qualifiers 1. 607 Corganism="Triticum aestivum" /organism="Triticum aestivum" /organism="Triticum" /organism="Triticum"	BASE COUNT 199 a 195 c 95 g 117 t 1 others ORIGIN Alignment Scores: 2.97

BASE COUNT 106 a ORIGIN	Alignment Scores: Pred. No.: Score:	Percent Similarity: Best Local Similarity Query Match: DB:	-10-048-	DD 196 ACCGGTTCGGC	Oy 28 ProLysAsnSea	Db 256 CCCCGAAGTACA	289	QY 68 GIUSELLYSALE ::::: Db 337 CGCCCTCGGTCI	Oy 88 AlavalSerLeu	Db 397 CGGTGCAGCTG	Qy 103 AlaArgThrGlu Db 457 CGACGGGTGCG	Oy 123 ThrValAsnAle	Db 517 CTCGCCTCCGC	z	ACCESSION BUB38004 VERSION BQB38664.1 KEYWORDS EST SOURCE bread whee	NISM		AUTHORS Altenbach, K., Cross	Wilson,C. TITLE The struct	genomes - JOURNAL Unpublishe		Fax: 51059 Email: oar Sequences quality se	Seg prime FEATURES
Db 177 GTATTGGCAACCACAACTACAGGAGCAGCAGCAGCAGCAGCAGCAGCA 236	Qy 22SerThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeu 39 ::: ::: :::	Qy 40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlnTyrTrpLys 59 Db 297CATGGATGTTGTATTGCAGCAACAACATAGGGATG 338	Oy 60 Ile74	75	399 ATGGCAGATCCCTGAGCAGTCGCAGGCCATCCACAATGTTGTTCATGCTAT	Qy 83 AspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsnProAsn 102 ::: ::	103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu	DD 504 CICCIIGCAACAGCICIGCAACAAIAICCAIIAGGCCAGGGCICCIICCG 554 Oy 123 Thrvalasnala 126		RESULT 25	DEFINITION 17000687509132 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449653777 5', mRNA sequence.	ACCESSION BM634463.1 GI:18933974	KEYWOKUS EST. SOURCE African malaria mosquito. ORGAN:S Anobeles gambiae	KEFERENCE 1 (Dases I to /14) AUTHORS HOLL, EAST, Lin, JJ., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab P. Colling B. Wonton I C. and Hoffman C. I.	TITLE Celera Anopheles gambiae EST project JOURNAL Uppublished (2002) COMMENT Contact: Holt R.A.	Celera Genomics 45 w Gude Dr., Rockville, MD 20850, USA mai - 24045-3151	lera.com	Seq prime	FEATURES Location/Qualifiers source 1.714	/organism="Anopheles gambiae" /strain="RSP-ST (Reduced susc. to Permethrin - std.	/db_xref="taxon:7165" /clone="19600449653777" /clone_lib="% .dam.ad.cDNA1" /dev_stage="Adult"	/lab_host="DH10b" /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1.	Not I site is 3'. Clones available through the Malaria Bacaarch and Baferance bacant Bacantar Contar

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Tucum aestivum

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
triceae; Triticum.
bases 1 to 808)
nbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin
crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,
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is have been trimmed to remove vector sequence and low
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ler: SK primer.
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/clone_lib_will_w. Ogihara unpublished cDNA library, Wh_e"
/tissue_type="seed DPA10"
/dev_stage="Feekes" scale 11.2"
/dev_stage="Feekes" scale 11.2"
/note="Wetcr: Lambda Uni_zAP XR, excised phagemid;
/note="Wetcr: Lambda Uni_zAP XR, excised phagemid;
Site_1: EcoRI: Site_2: XhoI: Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the pooled from the two
samples, polye pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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647 GTTGAGCCAAGTCTCCAACAACACAACAATA-----TCCATCAGGCCA 697
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/organism="Triticum aestivum"
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/db xref="taxon:4565"
/clone="whello22"
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Conservative:
Mismatches:
Indels:
Gaps:
   /organism="Triticum aestivum"
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Best Local Similarity:
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rcent Si st Local ery Matc : -10-048- 139 22 22 40 40 259	301 ATCACAAGTTTTGCAACAAGTACTTACCAGCTGTTGCAAGAATTGTGTGAACACCT 75	Db 466 CTCCTTCCAACACACAATATCCATTAGGCCAGGGCTCCTTCCG 516 Qy 123 ThrValAsnAla 126 ::::: Db 517 GCCATCTCAGCA 528 RESULT 29 BQ246932 LCCUS BQ246932 LCCUS BQ246932 LCCUS BQ246932 LCCUS BQ246932 CCCATCTCAGCA 528 ACCESSION BQ246932 VERSION BQ246932 CCCATCTCAGCA 528 ACCESSION BQ246932 CCCATCTCCG 516 ACCESSION BCA46932 CCCATCTCCG 516 BQ246932 ACCESSION BQ246932 ACCESSION BQ246932 CCCATCTCGCAGCA 528 ACCESSION BCA46932 ACCESSION ACCESSION BCA46932 ACCESSION ACCESSION BCA46932 ACCESSION ACCESSION BCA46932 ACCESSION ACCE	AUTHORS AUTHORS AUTHORS Cloutter,S TITLE Wheat functional genomics - Glenlea developing seeds CDNA libraries JOURNAL Unpublished (2002) CONDACT: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Daffoe RA, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fax: (204) 983-24604 Email: scloutiereem.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >1.4 kb Plate: 003 row: D column: 12 Seq primer: M13 Reverse. Location/Qualifiers Source //Organism="Triticum" //Organism="Triticum" //Clone="Table" //Clone="Table"
Db 625 ACAACAACAACAACAACAATTTTGCAACAATAACTGATTCCATG	RESULT 28 BE423599 LOCUS BE423599 LOCUS BE423599 LOCUS DEFINITION WHE0072_H10_02028 Wheat endosperm cDNA library Triticum aestivum ACCESSION BE423599 I GI:9421442 KERWORDS SEST 24-JUL-2000 WRNA sequence. VERSION BE423599 I GI:9421442 KERWORDS SEST 24-JUL-2000 KERWORDS REAUSH HE0072_H10_0202, MRNA sequence. ORGANISM Triticum aestivum ORGANISM Triticum aestivum Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta:	REFERENCE 1 (bases 1 to 536) AUTHORS Altenbach, S., Anderson, O.D., Chao, S., Galili, G., Han, P.S., Hsia (C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and TONG, J.C. TITLE The Structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library Upublished (200) COMMENT Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: \$10559518 Email: candersn@pw.usda.gov Sequence and bow quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.	Source 1. 536 Acganism="Triticum aestivum" Acganism="Triticum aestivum" Acganism="Triticum aestivum" Acganism="Triticum aestivum" Acganism="Triticum aestivum" Accone="Triticum aestivum" Accone="Web0072_H10_020" Aclone="Web0072_H10_020" Aclone="Web0072_H10_020" Aclone="Web0072_H10_020" Accone="Lib="Meate endosperm cDNA library" Accone="Lib="Meate endosperm cDNA library" Alignment Scores: BASE COUNT BASE COUNT

reverse

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AW448815

BRY_1500 BRY Triticum aestivum cDNA clone P52-1L, mRNA sequence.
AW448815
AW448815.1 GI:12019350
bread wheat.
                                       sequences generated with reverse with forward primer and 3' end).
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Site_1: Not1; Site_2: Mlu1; mRNA obtained from wheat see
of cultivar Gleniea 15 days post-anthesis"
a 197 c 103 g 123 t
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38
17
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51
               Email: scloutier@em.agr.ca
was cloned directionally, not all sequenc
primer were from the 5' end (same with fo
Average insert size 1s >1.4 kb
plate: 032 row: G column: 05
Seq primer: M13 Reverse.
Location/Qualifiers
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Indels:
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Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
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TaE15032G05R TaE15 Triticum aestivum cDNA clone TaE15032G05R, mRNA
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               Streptophyta; Embryophyta; Tracheophyta;
ta; Lilliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ValThralaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro---
                                             intlucture, introduction (bases) to 641)
Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm (npublished (2000)
Contact: Bryan Clarke
Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5000
Fax: 61 2 6246 5000
Fmail: bryancepi.csiro.au.
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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202 c 101 q 1
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Triticum aestivum
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                       /clone_lib="BRY"
                                                                                                                                                                                                                                               /cultivar="Wyuna
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 ORGANISM
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                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                   BASE COUNT
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/organism="Glycine max"
/db_xref="taxon:3847"
/clone_"Gm-r1083-2285
/clone_"Gm-r1083-2285
/clone_"Gm-r1083-2285
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/note="The library Gm-r1083 is a sequence-driven, reracked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 117 sequences from the progenitor library Gm-c1009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-c1013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from the progenitor library Gm-c1013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from the progenitor library from source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked Gm-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ennest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfspy/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: Incyte Genomics, 4633 World Parkway Litcle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reracking was performed by Incyte Genomics, St. Louis, http://www.incyte.com, and 3' sequencing by the Keck Center for Comparative and Punctional Genomics, University of Illinois, http://www.lie.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."
                                                                                                                                                                                                                                                                                                                          J. (bases, L.C. 041).
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other_ESTs: AW203461 corresponding to Gm-c1028-1497 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244 6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: 1-vodkin@uiuc.edu
GI:16343286
                                                                                                                                                                                                                                                                                                          (bases 1 to 641)
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Query Match: DB:	12.87% Indels: 26 . 13 Gaps: 8	Score: Percent Similarity:
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Db 130 ATCACATACA	ATCACATACACTACTACTATATAGCATACAATCTGTTCTTGCAGGGAGGCG 183	١.
Qy 24 ProGluserA Db 184 CCGGAAGAAG	ProgluserAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAla 43 :: CGGAAGAAGTTGACTGGGACATGGCGGAAATCTGGGATGCCTCATAAT 243	107
Ov 44 ValLysGlnT		Оу 25
244		Db 167 ACAACAACAAC
Ov 64 LystenSers	avor [5avor [4rhth] avor [7sv.	Oy 38 SerLeulleLy
	STJCJS ATAAATATGGATGT	227
Oy 81 ValAlaAspLysAlaPro	GluAlaValSerLeuThr	
Db 334 AGCACGCGG	AGCACGCGGGTCTCCAGCTTAACAGTGCCTGAATCCTCTCTCT	269
Oy 95 ThrThrAlaP		Db 329 GCACCTATGGC
3.94	ccicaaacgaic	Qy 81 ValAlaAspLy:
Oy 115 Ser 1 Db 448 TCTCACTAGG	SerLeuLysProCysMetLeuGluThrValAsnAlaPheile 128	389
SULT 33		Oy 101 ProAsnAlaArd
	3 641 bp mRNA linear EST 25-JUN-2002	434
DEFINITION BRY_1500	EST endosperm library Triticum aestivum cDN	Qy 121 LeuGluThrVa
z	3.1 GI:21555048	Db 485 CTTCCGGCCAT
NEIWOKUS EST. SOURCE bread wheat. ORGANISM Trificum aes	EST. Pried wheat. Prificum aperium	RESULT 34 BQ251877 100118 B0251877
	ta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	NOITI
	optimistophyti, magnitiophytia, militaria, foales, foaceae, foolueae ; Triticeae; Triticum.] (bases 1 to 641)	ACCESSION BQ251877 VFDCTON BO251877
AUTHORS Clarke, E	Clarke, B., Lambrecht, M. and Rhee, S. Assessing the utility of Arabidosis genomic information for	S
AL		NISM
COMMENT Contact: The Arab		Spermatop ; Tritice
Carnegie 260 Pana	Carnegie Institution of Washington, Dept. of Plant Biology 260 Panama Street, Stanford, CA 94305, USA	CE 1
Tel: 1 t Fax: 1 6	550 325 1521 x 251 550 325 3748	TITLE Wheat fund JOURNAL Unpublish
Ema11:	rhee@acoma.stanford.edu. Location/Qualifiers	
source	1. 541 /organism="Triticum aestivum"	
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	/Clone_ilb="Wheat ES! endosperm library" /tissue_type="endosperm" /dov stand="doveloning endosperm tissue 0 10 and 12 bbx	was clone primer we
	10 and 15	Averaye in Plate: 02: Seq prime
BASE COUNT 215 ORIGIN	a 202 c 101 g 123 t	FEATURES source
Alignment Scores: Pred: No.:	4.32 Length: 641	

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tier.s.

t functional genomics - Glenlea developing seeds cDNA libraries blished (2002)
act: Dr. Sylvie Cloutier
al Research Centre, Agriculture and Agri-food Canada
Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
(204) 983-2340
i. (204) 983-2340
i. (204) 983-4604
li: scloutierfemagr.ca
clonded directionally, not all sequences generated with reverse ner were from the 5' end (same with forward primer and 3' end).
rage insert size is >870 bp
primer: M13 Reverse.
Location/Qualifiers
l. .643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; pphyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideaeeae; Triticum.
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                                                                                                                                                                                                ysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
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  Matches:
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Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 25 days post-anthesis"
a 204 c 106 g 127 t
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ246079 647 bp mRNA linear EST 03-MAY-2002 TaE15016E10R TaE15 Triticum aestivum CDNA clone TaE15016E10R, mRNA
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Matches:
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Mismatches:
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                   BASE COUNT
                                                                                                                                                                           Pred. No.:
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/clone_lib="Table".
/tissue_type="developing seeds"
/tissue_type="developing seeds"
/dev_stage="l5 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glanla days post-anthesis"
197 c 105 g 128 t
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TaEl5 Triticum aestivum cDNA clone TaEl5039G10R, mRNA
                                                       with reverse and 3' end).
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                                                       sequences generated with forward primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 647
36
17
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53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE15016E10R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                    was cloned directionally, not all primer were from the 5' end (same Average insert size is >1.4 kb Plate: 016 row: E column: 10 Seq primer: M13 Reverse.
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                                                                                                                                             Location/Qualifiers
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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87.00
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sequence.
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Best Local Similarity:
Query Match:
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Wheat functional genomics - Glenlea developing seeds cDNA libraries Wheat functional (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RG, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-214604
Exar: (204) 983-4604
Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Tritlicene; Tritlicene; Tritlicene; Tritlicene; Tritlicene; Tolotherene; Tritlicene; Trit
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/dev_stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcwv-SPORT6.0 (invitrogen Technologies);
Site_1: NotI: Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"
204 c 104 g 127 t
                                                                                                                                                                                                                           BQ249968 652 bp mRNA linear EST 03-MAY-2002
TaE25011E12R TaE25 Triticum aestivum cDNA clone TaE25011E12R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TCCATTAGGCCAGGGCTCCTTCCG 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reprimer were from the 5' end (same with forward primer and 3' Average insert size is >870 bp Plate: 011 row: E column: 12 Seq primer: M13 Reverse.
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Mismatches:
Indels:

    .652
    /organism="Triticum aestivum"

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Matches:
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     437 CTCCTTCCAACAGCCTCTGCAACAATA----
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37.67
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                                                           123 ThrValAsnAla 126
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BQ249968.1
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                                                                                                                                                                                                       Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Coreal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-24604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 039 row: G column: 10
Seq primer: M18 Reverse.
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/tissue_type="developing seeds"
/lab.host="E. Coli DH10B"
/note="vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: Not1; Site_2: MluI: mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
a 207 c 106 g 128 t
                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
1 (bases 1 to 652)
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Mismatches:
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7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro-----
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AUTHORS
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-24604
Exa: (204) 983-4604
Email: scloutler@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="developing seeds"
/dev_stage="25 days after anthesis"
/dev_stage="25 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcWv-SPORT6.0" (invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"
a 195 c 104 g 136 t
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 657)
                                                                                                                                                                                                                                                                                                                        BQ249079 657 bp mRNA linear EST 03-MAY-2002 TaE25048C03R TaE25 Triticum aestivum cDNA clone TaE25048C03R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences generated with reverse with forward primer and 3' end).
                                                                                                      81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
                                                                                                                                    398 TAT------TATTCTGCATCAACAACAACAACAACAACAACAACTATCGAG 442
                                                                                                                                                                 ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120
                                                                                                                                                                                        338 GCACCTATGGCAGATCCCTGAGAAGTTGCAGTGCCAGGCCATCCACAATGTTGTTCATGC 397
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                                         ------CluThrAla------CysGlyCys
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/cultivar="Glenlea"
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/clone="TaE25048C03R"
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BQ249079.1
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BQ249079
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/tissue_type="developing seeds"
/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
/note="vector: pcMv-SPORT6.0 (Invitrogen Technologies);
Site_1: Not!; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 658)
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                                                                                                    81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
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                                                              ----GluSerAsnProLysAsnSerSerAlaAsnLeuThrThr 37
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63 GTATTCGCAACCACAACCAATTTCACAGCAGCAGCAGCAGCAGCAACAACAACAACA
                                                                                                                                                                                     SerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr
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Contact: Dr. Sylvie Coutier
Cereal Research Centre, Agriculture and Agri-food (195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Fax: (204) 983-2340
Email: scloutier@em.agr.ca

    658
    /organism="Triticum aestivum"

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BQ244737
BQ244737.1 GI:20440613
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FEATURES Location/Qu source 1674	/ Organism=" / Cultivar="t / db_xref="t / Clone="TaE / Clone="TaE / Clone="TaE / Line="TaE	Site_1: Note Site_1: Note of cultivar BASE COUNT 236 a 214 c	Scores: : imilarity: I Similarity: ch:	US-10-048-196-2 (1-134) x BQ2504 Qy 7 ValThralaThrLeuMetThra	Db 266 ACAACAACAACAACAACAACAACAA Qy 38 SerLeulleLysHisAlaValL	58 368 75	Db 428 GCACCTATGGCAGATCCCTGAG Oy 81 ValalaAspLysalaProGluA 188 TATTATT Oy 101 ProAsnAlaArgThrGluValA 19 533 CCAGGTCTCCTTCCAACAGCTT OY 121 LeuGluThrValAsnAla 126 Oy 121 LeuGluThrValAsnAla 126 Db 584 CTTCCGGCCATCTCAGCA 601 Search completed: May 5, 2003, Job time: 1069 secs
BASE COUNT 227 a 210 c 99 g 122 t ORIGIN	Alignment Scores: 4.52 Length: 658 Pred. No.: 87.00 Matches: 38 Scoret Similarity: 37.67% Conservative: 17 Best Local Similarity: 26.03% Mismatches: 51 Query Match: 12.87% Indels: 7 DB: 14 Gaps: 7	US-10-048-196-2 (1-134) x BQ244737 (1-658) Qy 7 ValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrPro 24 Dy 15-0	25 25 219 38 38 279	Oy 58 TrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer 74	81 ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn :::	<pre>Qy 101 ProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMet 120</pre>	RESULT 40 BQ250428 LOCUS BQ250428 BQ250428 LOCUS Tab25005B09R Tab25 Triticum aestivum cDNA clone Tab25005B09R, mRNA Sequence. ACCESSION BQ250428.1 GI:20446304 EST. Second BQ250428.1 GI:20446304 EST. SPETALICUM aestivum ENKAYOCES, VIIIIQUANCES, MAGNOLIOPHYTA; Embryophyta; Tracheophyta; SOURCE ORGANISM ENKAYOCES, VIIIICUM aestivum ENKAYOCES, Triticum aestivum ANTHOR, Contact, Triticum aestivum Contact, Dr. Sylva Cloutier Contact, St. Sylva Cloutier Contact, St. Sylva Cloutier Contact, Dr. Sylva Cloutier Co

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"Tab25005809R"
"Tab25005809R"
"Tab25005809R"
"Tab25005809R"
"Lype="developing seeds"
"Lype="developing seeds"
st="E. coli DH10B"
"Vector: pcMv-SPORT6.0 (invitrogen Technologies);
Vector: pcMv-SPORT6.0 (invitrogen Technologies);
Not1; Site_2: MluI; mRNA obtained from wheat seeds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAAGTACTTACCAGCTGTTGCAAGAATTGTGTTGTCA 427
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SUMMARIES

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Command line parameters:

-MODGIL-frame+p2n:model-DEV-x1h
-MODGIL-frame+p2n:model-DEV-x1h
-MODGIL-frame+p2n:model-DEV-x1h
-MODGIL-JUSPTOLOSPOOL/US10048196/runat_28042003_151439_5575/app_query.fasta_1.327
-QB-N_Geneseq_101002 -OPMT-fastap -SUFFIX-rng -MINMATCH-0.1 -LOOPGL-0
-LOOPEXT-0 -UNITS-bits -STAFT-1 -END*-1 -MATRIX-blosum62 -TRANS-human40 cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE-LOCAL -OUTFMT-pto -NORN-ext -HEAPSIZE-500 -MINLEN-0 -NAXLEN-200000000
-USFR-US10048196_GCM.1_1.200_@runat_28042003_151439_5575 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FCAPPOP=6 -FGAPEXT=7
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1 MMKILYVTATLMTAFTLASC......SLKPCMLETVNAFIVPTTR 134
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GenCore version
Copyright (c) 1993 - 2003
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Resul No	ult No.	Score	Query Match	Length	DB	ΩI	Description
	:	67	00	405	22		Moraxella catarrha
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                                                                                                                                                                                                                                                                            The invention relates to the Moraxella catarrhalis strain ATCC43617

BASB125 protein (AAB60646) and to DNA encoding it (AAF59800). The
Invention also relates to immunogenic fragments of the BASB125 protein,
expression vectors and host cells comprising BASB125 nucleic acids, the
recombinant production of BASB125, vaccine compositions comprising the
BASB125 protein or uncleic acid, an antibody against BASB125, therapeutic
compositions comprising the anti-BASB125 antibody, and a method of
identifying a Moraxella catarrhalis infection via the detection of
BASB125 proteins or antibodies. The vaccine compositions of the invention
are useful as prophylactic or therapeutic agents against Moraxella
catarrhalis infections in mammals, particularly humans. Moraxella
catarrhalis is a Gram negative bacterium frequently isolated from the
human upper respiratory tract, which is responsible for several
pathological conditions. It is responsible for about 15% of otitis media
cases in children (which can lead to temporary or permanent hearing
loss). It also causes pneumonia in elderly people, and sluusitis,
cases in children (which can lead to temporary or permanent hearing
loss). It also causes pneumonia in elderly people, and sluusitis,
cosocomial infections and, less frequently, invasive diseases. BASB125
proteins or nucleotides may additionally be used in screening for novel
antibacterial compounds, and in the diagnosis and steging of infections.
The present sequence represents DNA encoding the Moraxella catarrhalis
strain ATCC43617 BASB125 protein.
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                                                                                                                                                                                             New BASB125 polypeptide isolated from Moraxella catarrhalis for treating, preventing and diagnosing diseases associated with M. catarrhalis infection in mammals, e.g. otitis media in humans
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Query Match:
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as ottlis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                            Genomic library; bacteria; human upper airway; otitis medla; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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Scarselli
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                     LysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle
                                                                                                                                                                                                                                    Neisseria meningitidis ORF 108 partial DNA sequence SEQ ID NO:385
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Rappuoli I
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98US-0094869.
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Tettelin H, Venter JC;
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, Pizza M,
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polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseriab bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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262 ATCGTCAAAAATGGCGGTAGAAAGCCAATGCGAATTGAACAAACGCAGCGAATGG 321
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Best Local Similarity:
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98US-0083758

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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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Ratti G,
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, Pizza M, Rappuoli R,
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                                                                         980S-0103749.
980S-0103794.
980S-0103796.
990S-0121528.
98US-0094869.
98US-0098994.
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Tettelin H, Venter JC;
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Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B: against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent specifically claimed Nelseria meningitidis genomic DNA agequences. AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Nelsezria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81321 represent PCR primers used in the isolation of Nelsezria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Nelsezria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Nelsezria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 102634 BP; 23871 A; 24828 C; 27888 G; 26042 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                               N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
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C, Mora M,
                                                                                                                               AAA81464 standard; DNA; 102634 BP.
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99US-0132068
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Rappuoli R, Pizza M;
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119 Cys 119
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30-APR-1999;
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                                                                                      RESULT
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                                                                                                                                                                                                                                        Masignani V, Mora M;
Scalato E, Scarselli
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Scarlato V;

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                                                                                                          60485 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGGCTGC 60435
                                                                                                                                                   GCCGCCGGAGGCGGTAACACATTCGGCAGCTTAGACGGTGGCACAGGCATGGGCGGCAGC 60375
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Rappuoli R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections ^{\rm -}
                                                                                                                                                                                                                                                                                                       IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro 118
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                                                                                                                                                                                                                   LysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCys 78
                                                                                    MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                         LeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp
                                                                                                                                                                                                                                                              GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla
                                                                                                                               AlaSerThrProGluSer----AsnProLysAsnSerSerAlaAsnLeuThrThrSer
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Scarlato V,
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 Matches:
Conservative:
Mismatches:
Indels:
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Galeotti C, Mora M, Ratti G, Scarselli M,
Frazer CM, Grandi G;
                                                                US-10-048-196-2 (1-134) x AAA81464 (1-102634)
                                             Gaps:
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ID AAF21609 standard; DNA; 349980 BP.
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          Percent Similarity:
Best Local Similarity:
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Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF215607 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21608 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have attained and an each of a minbacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which bluds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial activity or as a diagnostic reagent to Neisserial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
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                                                                     present invention describes the full length genome
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Claim 7; Appendix A;
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                                                                     The
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

Crepresent specifically claimed Neisseria menigitidis genomic DNA sequences; AAA81260 to AAA812620 to AAA825663 represent corresponding proteins; AAA81254 to AAA81259 and AAA81301 represent PCR primers used in the sequences; and AAA8132 to AAA81452 represent Meisseria menigitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria menigitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria menigitidis MenB polynuclectide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences; protein sequences, and antibodies gainst them, can be used in the manufacture of a composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; condyor against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious CM Melivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete conserved proportanically or an integer conserved from which may be presumed targets for the immune system and which was not antigened or surface exposed proteins that may be presumed targets for the immune system and which was not antigened or surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scarlato V;
                                                               Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1437668 BP; 344338 A; 353206 C; 385074 G; 355045 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable or at least more conserved than
                  N. meningitidis B full length genome DNA sequence SEQ ID NO:1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tettelin H, Venter JC;
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 866-1272; 1760pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frazer CM, Hickey E, Peterson J,
Masignani V, Galeotti C, Mora M,
                                                                                                                                                                                                                                                                                             99WO-US23573
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99US-0132068
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                                                                                                                                                         Neisserla meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ν, Gale.
P. Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-318079/27.
                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                                                                                                   WO200022430-A2
                                                                                                                                                                                                                                                                                          08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                       09-0CT-1998;
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                                                                                                                                                                                                                                              20-APR-2000
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Length: Matches: Conservative: Mismatches: Indels: 27.7 116.00 46.28% 23.97% 17.16% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Score:

US-10-048-196-2 (1-134) x AAA81490 (1-1437668)

Gaps:

Db 1064196 ATGAATAAAACCTTGTCTATT-----TTGCCGGTGGCAATCTTACTCGGCGCTGC 1064146 1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys 20 ò

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Db 1063908 CTGGCTCCGTCCACGCGAATCAGGCACTTGCCGCCCTGACGCCCAAAACGGTTTCCGCC 1063849
                           Db 1064145 GCCGCCGGAGGCGGTAACACATTCGGCAGCTTAGACGGTGCCACAGGCATGGGCGGCAGG 1064086
                                                                                                                                         Db 1064025 CGTTTGACCGCCTGCCGATGACTGCCGAAAAACAGGCGGAGTGCGAAAAACAAGATTTGC_1063966
                                                                                                                                                                                                   Db 1063965 GCTTGCGTCGCCCAAGAACCGAACGGATGACCGGCAACGATGTG---ATGCAGATG 1063909
                                                                                       Db 1064085 ATCGTCAAAATGGCGGTTGGGAGCCAATGCCGTGCGGAATTGGACAAACGCAGCGAATGG 1064026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scalato E, Scarselli M;
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21 AlaSerThrProGluSer----AsnProLysAsnSerSerAlaAsnLeuThrThrSer 38
                                                           39 LeulleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrp 58
                                                                                                                       59 LysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCys 78
                                                                                                                                                                                  79 GlyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAla 98
                                                                                                                                                                                                                                               99 IleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria gonorrheae ORF 108 partial DNA sequence SEQ ID NO:381
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Ratti
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 319; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      AAZ53215 standard; DNA; 519 BP
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98US-0094869.
98US-0098994.
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99US-0121528
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Tettelin H, Venter JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrheae
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P-PSDB; AAY74453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ53215;
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and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, and compositions of immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypurcleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
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262 GTCAAAATGACGGTAGAAAGCCAATGCCGTGCGGAATTGGACAGGCGCAGCGAATGGCGT 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae; S. pneumoniae; genome; diagnosis; assay; able medium; vaccine; pharmaceutical composition; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae genome fragment SEQ ID NO:28.
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Matches:
Conservative:
Mismatches:
Indels:
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110.50
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21.678
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                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) the nucleotide sequences at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae. The present invention also describes an isolated nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the inbrary which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating menna, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification molecules whose nucleotide sequence is homologous to amplification the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences: The computer readable medium can be used in a computer based system for identifying fragments of fragments of fragments of commercial importance, or primers are acid and produced produced computer based system for identifying fragments of fragments of commercial importance, or primers acid molecules whose necessary of the sequences. The computer fragments of fragments of fragments of commercial importance, or primer acid molecules whose necessary of the sequences of commercial medium can be used in a computer based system for identifying fragments of fragments of commercial medium can be used in a computer based system for identifying fragments of fragments of fragments of commercial medium can be used in a computer based system for identifying fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical compositions and vaccines for S. pneumoniae.
     Fannon M;
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28
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38
15
     Dougherty BA,
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Conservative:
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Dillon PJ,
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                             Rosen CA;
     Choi GH,
                                                                           WPI; 1998-272225/24.
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  SC,
CA,
                                                                                                                                                                                                                pneumoniae
  Barash
Kunsch
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4776 ATGGACAGTAAGGTCAACCCGTTTATAAGAACTCAAGCAGCAAAGGCTATAGAACAA 4717

4716 TCTTATAAG 4708 SerLeuLys 117

RESULT 10 AAN90096

115

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3312 -----TATTCTGCATCAACAAAAAACAACAACAACAACGACGAGCCAGGT 3359
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                                                                                        3411 GCCATCTCAGCA 3422
                                                                         123 ThrValAsnAla 126
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                                                                                                                                      AAD08348 standard;
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                                                                                                                                                                                                                                                                                                                       The preferred gene fragment in the patent of the invention encodes alpha-gladin or glutenin, and the preferred plasmid encoding alpha-gliadin is PAY 31. The plasmid may be used for the prodn. of alpha-gliadin, which may be used in the food technology industry to modify prodn. processes of doughs and batters and to reduce unit costs. Gliadin may also be used for diagnosis and treatment of illness caused by wheat gluten proteins and for testing theories of dough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 IleLysHisAlaValLysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ile-----AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSer----
                                                                                 Coeliac disease diagnosis; dough formation; food technology; ds.
                                                                                                                                                                                                                                                                      New wheat gluten protein gene plasmid - useful for genetic transformation of yeasts to produce gliadin or glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                Litts JC
                                                            Sequence of plasmid pAY31 encoding wheat alpha-gliadin.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                               Neill JD,
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  BP
AAN90096 standard; cDNA; 6978
                                                                                                                                                                                                          (UYHA-) UNIV OF HAWAII (USDA)
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Best Local Similarity:
Query Match:
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                                                                                                                         US4826765-A
                                         22-MAR-1991
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                                                                                                                                                                                                                               Greene FC,
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                    AAN90096;
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AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03997 represent the proteins they encode. AAE03948-AAE03996 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotrasis; food additive; gene therapy; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein-encoding gene 4 cDNA clone HBMBD51, SEQ ID NO:14.
                                                                                             3360 CICCTICCAACAGCCICIGCAACAATA-----TCCATTAGGCCAGGGCICCTICCG 3410
103 AlaArgThrGluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a //product= "Human secreted protein precursor" //tranal_except= (pos:524..526, aa:Xaa) //note= "Xaa equals any of the naturally occurring L-amino_acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; proliferative disorder;
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pharmaceutical; gene; ss. Drosophila melanogaster.

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treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the innume specific and include developing products for the diagnosis or treatment of proliferative disorders for the diagnosis of the immune system, alboy autoimmune diseases (e.g., rheumatoid arthritis), inflammation, albus, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, naglogenic disorders, and infections. The proteins can also be used to aid wound healthy and epithelial cell proliferation, to prevent skin aging due to subturn, to maintain organs before transplantation, for supporting cell
                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                            culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.
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Drosophila; developmental biology; cell signalling; insecticide;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 10073; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                       Li PWD,
                                                                                                                         23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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84.50
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Best Local Similarity:
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                                                                                         27-SEP-2001
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                        3794 CGAATCCACCACCAGTTCCATCACAGACTTGGCCCGACTGGAGAAGATGAAGGTCTCTGA 3735
                                                                                                                                                                                                                                                                                                                                                                        3734 CCTAAAGCAGCATCTCAAGCAGCAGCAGTTGCCCGTTTCCGGTCCTAAACCACATCTGAT 3675
                                                                                                                                                                                                                                                                                                                                   107 -ValAlaGlnLysIleValArgHisSerLeu-------LysProCysMetLe 121
     53 ThrGlyHisGln-TyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLy 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus DNA for cellular proliferation protein #423.
                                                                                                           72 sIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuTh
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                                                        3812 TCCGCCACCAGCTAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
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16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABR32072).
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                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 10070.
                                                                                                                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
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ABL05196 standard; cDNA; 6959 BP
                                    1602 TGAGAGGCTGAAACCGTATCTG 1623
121 uGluThrValAsnAlaPheIle 128
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11-JUL-2000; 2000US-0614150.
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Source: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                             MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAla------PheThr 16
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                                                                                                                                                                                                                                                                                                            27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln
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Matches:
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22-DEC-2000;
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                                                                                                                                                                           Query Match:
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the willowlybublished_pct_sequences.
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                                                   G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 AGAGCTTTTCTAAATTCTACAGGTGATAAATATTGGCCAGTTGTGTGTCTTGGATCGACG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAla-------PheThr 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 TTAATCCAGTCAGGCAAATCTCTAAAGCGCGTGATATTTGGACGAATTGCACCTCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet-----Lys
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                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 957 BP; 335 A; 141 C; 194 G; 287 T; 0 other;
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34
119
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Matches:
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                                                                                                                                                                                                                                                                                   Claim 27; Seq ID No 8609; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 LeuAlaSerCysAlaSerThr-------
                                                   Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-048-196-2 (1-134) x AAS54972 (1-957)
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84.00
45.30%
29.06%
12.43%
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(ELIT-) ELITRA PHARM INC.
                                                 Ohlsen l
Xu HH;
                                                                                                                             2001-611495/70.
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                                              Haselbeck R,
Yamamoto RT,
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US-10-048-196-2 (1-134) x AAV74758 (1-1799)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunsch CA;
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                                                                                                                                                                                                     Staphylococcus aureus contig SEQ ID #447
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1141..1200
/*tag= a
/note= "these bases
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AAV74758 standard; DNA; 1799 BP
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                                                                                                                                   (first entry)
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Conservative: Mismatches: Indels:

12.1 84.00 45.30% 29.06% 12.43%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Matches: Length:

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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scalato E, Scarselli M;
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                                                                                                                                                                                             --- PheThr 16
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                                                                                     606 TTAATCCAGTCAGGCAAATCTCTAAAACGTGTGATATTTGGACGAATTGCACCTCGGAAA
                                                                                                                                                546 TGACCTAAATCAAATTCATAATCATACGTGCATCAATAATGACTGTGATCATCATCAT
                                                                                                                                                                           47 ThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMet-----Lys
                          663 ATGCCACCAGTACAGTACGTAACC --- ACTITITITATCTGCAAATAACGCTTTATTCTCT
                                                                                                                   27 AsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGln
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                                                                                                                                                                                                                                                                                                               85 Ala -- - ProGluAlaValSerLeuThrGluLeuThrThrAlaAlaIleAsn 100
1 MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAla-
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Ratti G,
                                                         17 LeuAlaSerCysAlaSerThr-------
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Rappuoli R,
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98US-0094869.
98US-0098994.
98US-0099062.
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Petersen J, Pizza M, F
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrheae
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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Page 13

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20-APR-2001; 2001WO-US12865.

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represent
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AA254537 to AA25456 and AA254616 to AA255473 repress PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrTrpLys1leAlaAlaMetLysLeuSerSerGluSerLysAlaLys1leSerGluThr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein encoding DNA #64.
                                                                                                                                                                                                                                                    Sequence 1731 BP; 507 A; 521 C; 418 G; 285 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 ACGCCGCCGACAGCGCAAGCAAAAAGGCAACGTTGACG-----
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Mismatches:
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36.438
23.268
12.068
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Best Local Similarity:
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01-NOV-2001

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Propionibacterium acres immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acres. The disorders include SAPHO syndrome (synovitis, acre, pustulosis, hypertosis and osteomyelitis), uveltis and endophthalmitis. P. acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P. acres in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient comprises contacting a sample with a binding agent, that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypetides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU55305-AAU55603 and AAU67567-AAU67570.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1708 TCCAAGGCC-----GTCGAGACGGCGACAAAGTGCTTAGCGACGGCGTCACGTCGAGGC 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACCCAGCTCCAGAACCCAAAGGCGTTCACTGGGTCGATGCCGAACTCCTCGACCTTG 1707
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                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrThrSerLeuIleLysHisAlaValLysGlnThrCysGln------ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLysalaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAla 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1588 TTCGGCCCGATCGCGACGGCAAGCGACGTACCGACGCGGAATCCACCGAGTATCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ThrLeuAlaSerCysAlaSerThrProGluSerAsnProLysAsnSerSerAlaAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29139 BP; 6272 A; 9455 C; 8116 G; 5292 T; 4 other;
                                                                                                                                                                                Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
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                                                                                                                                                                                Wang SS,
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 64; 1069pp; English.
                                                                                                                                                                           DH, Mitcham JL,
nng Y, Jen S, C
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                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                   L'maisonneuve J,
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Sequences AASS9506-AASS9804 represent DNA molecules encoding

Propionibacterium acnes immunogenic polypeptides. The proteins and their

Expectated DNA sequences are used in the treatment, prevention and

diagnosis of medical conditions caused by P. acnes. The disorders include

Cashelo syndrome (synovitis, acne, pustulosis, hypertosis and

Osteomyelitis), uveltis and endophthalmitis. P. acnes is also involved

in infections of bone, joints and the central nervous system, however it

Cs sparient comprises contacting and the presence or absence of P. acnes in

cvulgaris. A method for detecting the presence or absence of P. acnes in

cy vulgaris. A method for detecting the presence or absence of P. acnes in

content comprises contacting a sample with a binding agent that binds to

the proteins of the invention and determining the amount of bound protein

in the sample. The polypeptides may be used as antigens in the production

consed to downrequlate expression and activity of P. acnes polypeptides and

therefore treat P. acnes infections. The antibodies can be

consed to downrequlate expression and activity of P. acnes polypeptides and

therefore treat P. acnes infections. The antibodies may also be used as

diagnostic agents for determining P. acnes presence, for example, by

contact inkeed and immunosorbent assay (ELISA). This sequence encodes the

colypeptides shown in AAU55305-AAU55603 and AAU67567-AAU67570.

Note: The sequence data for this parent did not form part of the printed

specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveltis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                  1822 CACCGGGCA-----TTGGTCAGAGTCTCCAAAGTGGTGAAGGTCTTAGAGGCAATGATG 1875
89 ValSerLeuThrGluLeuThrThrAlaAlaIleAsnPro-----AsnAlaArgThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                          1762 recresergrescantescancescancesaccanecercanseascancecacs
                                                                                        GluValAlaGlnLysIleValArgHisSerLeuLysProCysMetLeuGluThrValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein encoding DNA #64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhatia A;
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Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 64; 1069pp; English.
                                                                                                                                                                                                                                                                                                                     AAS59569 standard; DNA; 29139 BP.
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; 2000US-208841P.
; 2000US-216747P.
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L'maisonneuve J,
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02-JUN-2000;
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19713 CTCACGATTTATAGATTAAGGCTCTGCTCAAGTAGGGAAGAGTCACAACGCCGAGCGTCG 19654
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                                                                                                                                                                                                                                                                                                         19482 AACCGTTTAAGGAACCCAGCACAAAGGCCCCGCCCTCCATAGCCATCAGC------TTG
                                                                                                                                                                                                                                      44 ValLysGlnThrCysGln-----ThrGlnLeuThrGlyHisGlnTyrTrpLysIle
                                                                                                                                                                                                                                                                                                                                             AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                ------ValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThr
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                                                                                                                                                                                   12 MetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnProLys--
                           Sequence 29139 BP; 6272 A; 9455 C; 8116 G; 5292 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #15441.
                                                                 Length:
Matches:
Conservative:
Mismatches:
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                      Indels:
                                                                                                                                   Gaps:
                                                                                                                                                          US-10-048-196-2 (1-134) x AAS59569 (1-29139)
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                                                                1.24e+03
81.00
47.15%
25.20%
11.98%
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG15450.
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                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                     Alignment Scores:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or blological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and considers of the invention invention which in a call sequences. Askedled trapresent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed
from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2011 AGTGTGTCCTGCACAATACCCATGACAGGCCGATTGCTCTGGGGGGGTGACAATCATGCGA 1952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2128 TTTAGGATGGCCGGCTGTGGGACCTTCCCATCCCACGTCGACAGGAACATCAGGAGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------LeuSerSerGluSerLysAlaLysIleSer-GluThrAlaCysGlyCysVa
                      mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA differentially expressed in granulocytic cells #1187.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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viral infection; parasitic infection; protozoal infection;
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                                                                                                    Claim 1; SEQ ID No 15441; 103pp; English.
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response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrom, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection fungal infection and M5 is from GS in the tissue. MI is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel digease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. of the printed specification, but was obtained in electronic format directly from WIPO at infection; sterile inflammatory disease; psoriasis; BP; 1512 A; 2090 C; 1685 G; 1445 T; 0 other; Note: The sequence data for this patent did not form par Vockley J; 24 Weissman SM, Yamaga S, Matches: Length: ftp.wipo.int/pub/published_pct_sequences Claim 1; SEQ ID No 1187; 114pp; English. 03-OCT-2000; 2000US-237189P. 03-OCT-2001; 2001WO-US30821 80.00 46.32% (GENE-) GENE LOGIC INC WPI; 2002-435328/46. Beazer-Barclay Y, WO200228999-A2. Sequence 6732 drug toxicity Homo sapiens. 11-APR-2002.

Conservative:

Percent Similarity:

us-10-048-196-2.rng

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                        ||| :::||| ||| ||| :: ||| ||| 3128 TTAGGATGGCCGGCTGTCGACACGAACATCAGGAGGTTC 2069
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medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                          45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLys
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                                                                                                                                                                      ---SerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaVal
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 Mismatches:
Indels:
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                                                                  US-10-048-196-2 (1-134) x ABK84616 (1-6732)
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Best Local Similarity:
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a food supplement. (II) and its binding partners are useful in medical limaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
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30-APR-1999;
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ABK35351 standard; cDNA; 2456

RESULT 24 **ABK35351** (first entry)

38-MAY-2002

ABK35351;

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proteins its in reisseria genuite sequences, Analysis, to Analysis, to proteins its in reisseria genuite Sequences. Analizably Claimed Neisseria meningitidis genomic DNA sequences and their corresponding proteins; Analizable to Neisseria DNA sequences and their corresponding proteins; Analizable to Analizable and Analizable is protein sequences; and Analizable to isolation of Neisseria meningitidis DNA sequences; and Analizable Corresponding proteins of in the sequences; which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used in the manufacture of a composition can be used in the manufacture of a composition of the treating, preventing or in the manufacture of a medicament for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenia Neissariae. Identification of sequences from the bacterium will also facilitate production of bological probes,
  Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system a which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance.
                                                                                                                                Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                            j immunogenic
to AAA82414
  Scarselli M,
                                                                                                                                                                                                                                                                                                         The present invention describes methods of obtaining proteins from Neisseria genomic sequences. AAA81453 t
  Ratti G,
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  Mora M,
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  Galeotti C,
                                                                              WPI; 2000-318079/27.
Masignani V,
                             Rappuoli R,
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Sequence 783 BP; 214 A; 203 C; 197 G; 167 T; 2 other;

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LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluvalAlaGlnLysIleValArg 113
                                                                                                                                                                                                                                                                                 140 TCCACCCACAAATAAAAAACGGCCCAAAACCAGCATGACTGCAACACTCAAGGGGTTA 199
                                                                                                                                                                                                                                                                                                                                                                                               ATCACGGCGCCGCAGGTATAAAAGCAATGGCAAGATTAAGGACGAAGCGGTTGGCTTTCCGG 298
                                                                                                                                                                                                                           TCAATCGGACGCAATGCATCAACATCGGCAATTTTAGGCTCTGCTCGGCTTTGGCGTTTC 139
                                                                                                                                                                                                                                                                                                            24 ProGluSerAsnProLysAsnSerSerAlaAsnLeu---ThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                 43 AlaValLysGlnThrCysGlnThrGln-----LeuThrGlyHisGlnTyrTrpLysIle 60
                                                                                                                                                        61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
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US-10-048-196-2 (1-134) x ABK35351 (1-2456)

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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the dentification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), lingammatory disorders (e.g. Alzheimer's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of
                                                                                                                        viral infection; bacterial infection; fungal infection; diabetes; astima; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer; disease; parkfinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis and for treating myeloid or lymphoid cell deficiencies. Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Resnick RJ;
                                                                                                        gene; ss; nutritional supplement;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel K,
                                                                       Human cDNA encoding secreted
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K, Graham JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more.genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
             1876 TGAAGAAGTCCATGTGGGGTCAGTTCTGGTCTTCCACCAGGTTCTTCAAATACTTAT 1935
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                                                   1936 GCATAGCATCCAAAGTTAAAAGGGTTGTGCAACTAGCTCGAGAGGAAATCAAGAATGGAA 1995
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                                                                                                                                                                                                          79 lyCysValAlaAspLysAlaProGluAlaValSerLeuThrGluLeuThrThrAlaAlaI 99
                                                                                  Ser-LeulleLy
                                                                                                                                                                 sile-AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysG
                                                                                                                                                                                                                                                  99 leAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg-HisSerLeuLysPro
MetMetLysIleLeuTyrValThrAlaThrLeuMetThrAlaPheThrLeuAlaSerCys
                                                                                                                                                                                                                               -----ACATTAGAAGCTTTGGAAGAGGGCGGGG
                                                                                                                         sHisAlaValLys-----GinThrCysGlnThrGlnLeuThrGlyHisGlnTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 10190.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 10190; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                        2125 ATTTTCCTGCTCCAGACAAAAAAACTTTATAGTT 2160
                                                                                                                                                                                                                                                                                           119 Cys---MetLeuGluThrValAsnAlaPheIleVal 129
                                                                                -----AsnProLysAsnSerSerAlaAsnLeuThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                        ABL05236 standard; cDNA; 10867 BP
                                       21 AlaSerThrProGluSer------
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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P-PSDB; ABB61133.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4336 GGGGCGAGGATGCAGGAGGTCGTCTGTGGGGTAATTACGGACAAGTGCGCACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 --- AlaLysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 SerSerAlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnLeuThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                       Sequence 10867 BP; 3008 A; 2450 C; 2315 G; 3094 T; 0 other.
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Matches:
Conservative:
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2000US-0649167
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P-PSDB; ABG07375.
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23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain excending in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and configuratic coding sequences of the invention.

Sequences AAS64197-AAS94564 represent novel human but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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Conservative:
Mismatches:
Indels:
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening
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28-SEP-2000;
Homo sapiens.
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Soppet DR,
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an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, obesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, cacinoma, clear cell cancer, infiltrating ductal cancer infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                                   Sequence 14770 BP; 4829 A; 3240 C; 3211 G; 3490 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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2000US-209531P.
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79.50
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in capression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating cancer.
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25-SEP-2000;
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Soppet DR,
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Sequence 14770 BP; 4829 A; 3240 C; 3211 G; 3490 T; 0 othqr;

Alignment Scores:

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Tue May

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11890
 stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                        11950 AGGGAT------AACATAATT------GCACTTAGAAAAGCATGTGCCACACAAAAG 11994
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                                                                                                                                                   53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys 72
                                                                              14 AlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro---LysAsnSerSer 32
                                                                                                                 33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                                                                                                                      73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                     cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                   Kidney cancer related gene sequence SEQ ID NO:6875.
        Matches:
Conservative:
Mismatches:
Indels:
Length:
                                            Gaps:
                                                            US-10-048-196-2 (1-134) x ABL68257 (1-14770)
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20000S-234034P.
20000S-234052P.
20000S-234509P.
20000S-234569P.
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2000US-233617P.
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                Percent Similarity:
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S-SEP-2000;
S-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in comprises is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, calcar cell cancer, infiltrating ductal cancer, affiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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2000US-237172P.
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Best Local Similarity:
27-SEP-2000;
28-SEP-2000;
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28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                           12112 ACTACCACCACCACCAGCTGCACAGTTAAAGTTAGGAAAAGTCAGCTCAAGGAAGTATGT 12171
                                       11950 AGGGAT-----AACATAATT-----GCAGTTAGAAAAGCATGTGCCACACAAAAG 11994
                                                                                                           93 GluLeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleVal 112
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33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                 53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; dlagnostic; genetic disorder; ss.
                                                                                                                                                                    73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG00972.
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and to produce other types of data and products dependent on Di
amino acid sequences. AASG4197-AAS94564 represent novel human
diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the
specification, but was obtained in electronic format directly
                                                                                                                                                                                     Sequence 14797 BP; 3493 A; 3212 C; 3266 G; 4826 T; 0 other;
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P-PSDB; ABG21944.
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23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reacting disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in componsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic codding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11964 AGGGAT-----AACATAATT-----GCAGTTAGAAAAGCATGTGCCACACAAAAG 12008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 IleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeuThr 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 AlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro---LysAsnSerSer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 AlaAsnLeuThrThrSerLeuIleLysHisAlaValLysGlnThrCysGlnThrGlnLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 ThrGlyHisGlnTyrTrpLysIleAlaAlaMetLysLeuSerSerGluSerLysAlaLys
                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15187 BP; 4913 A; 3361 C; 3318 G; 3594 T; 1 other;
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Mismatches:
Indels:
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                                                                                                                                       Claim 1; SEQ ID No 21935; 103pp; English
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43.81%
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11.76%
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                                                                                         biodiversity
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ID AAA8
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414
represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81303 and AAB25620 to AAB2563 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis MenB polynuclectide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition can be used in the manufacture of a composition can be used in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B: against all serotypes; and/or against all asthogenic Neisseriae. Identification of sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and
                                                                                                                                                                                                                                                                                                                                                                                                                     Scarlato V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which are not antigenically variable or at least more conserved than
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          partial DNA sequence gnm_27 SEQ ID NO:27. ₹
                                                                                                                                                                                                                                                                                                                                                                                                 Tettelin H, Venter JC;
Ratti G, Scarselli M,
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Indels:
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C, Mora M,
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79.50
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Rappuoli R, Pizza M;
                                                                                                                                     Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-318079/27.
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                N. meningitidis
                                                                                                                                                                         WO200022430-A2.
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30-APR-1999;
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The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 from AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 4980 bp (i.e. the last 49980 bp of AAF21644 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21640 are repeated the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therappy.
                                                                                                              65624 TCCACCCACAAAAAAAAAAACGGCCCAAAACCAGCATGACTGCAACACTCAAGGGGTTA 65683
                                                                                                                                                                                                                                                                    65723 ATCACGGCGCGCAGGTATAAAAGCAATGGCAAGATTAAGGACGAAGCGGTTGGCTTTCCGG 65782
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Rappuoli R;
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                                                                                                                                                                                                                                94 LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg 113
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                                                                                                                                                        -----CysValAlaAspLysAlaProGluAlaValSerLeuThrGlu 93
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frames are used to detect, treat and prevent Neisserial infections
AlaValLysGlnThrCysGlnThrGln-----LeuThrGlyHisGlnTyrTrpLysIle
                                    65564 TCAATCGGACGCAATGCATCAACATCGGCAATTTTAGGCTCTGCTTGGCGTTTC
                                                                          61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
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Scarlato V,
                                                                                                                                                                                Peterson J, Tettelin H, Ratti G, Scarselli M,
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                                                                                                                                                                                                                                                                                                                                                65783 TCTTTTCCCAAGCCGTGC 65800
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                                            114 HisSerLeuLysProCys 119
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 115623 TCAATCGGACGCAATGCATCAACATCGGCAATTTAAGGCTCTGCTCGCTTTGGCGTTTC 115564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 115563 TCCACCCACAAAATAAAAAAACCGCCCAAAAACCAGCATGACTGCAACACACTCAAGGGGTTA 115504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 115683 CCCGAACGGGACGTACCCGGAACCAGTGCAAACACTTGGGCAACGCCGATCATCAAGGCA 115624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; ensyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ProGluSerAsnProLysAsnSerSerAlaAsnLeu---ThrThrSerLeuIleLysHis 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 LeuThrThrAlaAlaIleAsnProAsnAlaArgThrGluValAlaGlnLysIleValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly: --
                                                                                                                                                                                                                  Sequence 349980 BP; 84410 A; 84863 C; 94187 G; 86520 T; 0 other;
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Mismatches:
Indels:
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Matches:
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2000US-208841P.
2000US-216747P.
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79.50
40.578
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Best Local Similarity:
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07-JUL-2000;
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AAS59666/
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Alignment Scores:
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AAS68171/c
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                                                                                                                                                                                                                                                    Sequences AAS59506-AAS59804 represent DNA molecules encoding associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acres. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acres. The disorders include osteomyelitis), uveitis and endophthalmitis. P. acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigonis in the production of antibodies specific for P. acres proteins. These antibodies can be used to downregulate expression and activity of P. acres polypeptides and therefore treat P. acres infections. The antibodies may also be used as diagnostic agents for determining P. acres presence encodes the polypeptides shown in Adw05346 Adw05365 and Adw07770.

Note: The sequence data for this patent did not form part of the printed processing the contact of the printed presence of the printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  739 TGCGCACTGGACTCAACTTCACCGAGCGTGGCTTCGGTGTCCGCGGCGCCGTCGGGGTCT 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 TCTTTGGACAACTGGGAGTGCGATGGCTACACACGGAGGCATCTACGCCGCCCTTGTCAC 560
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                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AlaThrLeuMetThrAlaPheThrLeuAlaSerCysAlaSerThrProGluSerAsnPro 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 LysAsnSerSerAlaAsnLeu------ThrThrSerLeuIleLysHisAla 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 ValLysGlnThr------CysGlnThrGlnLeuThrGlyHisGlnTyrTrpLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     787 ACGACCAGTTCATCACCTGGGTGCCCTCTGACGGAGTCGGCCGCACAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AlaAlaMetLysLeuSerSerGluSerLysAlaLysIleSerGluThrAlaCysGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------CysValAlaAspLysAlaProGluAlaVal
                                                        Wang SS, Bhatia A;
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Mismatches:
                                                      Mitcham JL, Wang S:
Jen S, Carter D;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The conditions are ealso used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical ciscapted and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human
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printed
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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                                                                                                  126 AlaPhelleValProThrThr 133
                                                                                                                                               508 GCACCGTTATCTCCTACGACCTCA 485
                                                                                                                                                                                                                                                                                                                     AAS68171 standard; cDNA; 3300 BP
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG03984.
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2591 CTTTCCTCACATCAACATTGATGGGCTCCATCAGAGTAACCTTTGCAGGAGTAGCATGCAGG 2532
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                                                                                                                                                                              --- Val 44
                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                              91
                                                                           ---ThrLeuAlaSerCysAlaSer 22
                                                                                                                                                                                                                                ---TrpLys
                                                                                                                                                                                                                                                                             --SerGlüSerLysAla
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                                                                                                                           23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle----
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                                                                                                                                                                                                                                                                                                                                                                             ----ThrGluLeuThrThrAlaAlaIleAsnPro 101
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  Mismatches:
Indels:
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                                                                         5 LeuTyrValThrAlaThrLeuMetThrAlaPhe---
                          Gaps:
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                                                US-10-048-196-2 (1-134) x AAS68171 (1-3300)
                                                                                                                                                                                                                                                                             ---IleAlaAlaMetLysLeuSer---
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ID AAS70249 standard; cDNA; 3300
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23-AUG-2000; 2000US-0649167
 26.67%
11.69%
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P-PSDB; ABG06062.
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Best Local Similarity:
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             Query Match:
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Coding sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2351 CACGTAGAATCCATGCACTTATCGTATTCTTGTTCAGTGGGAGATCCAGATGGGAATGAG
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Matches:
Conservative:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynucleotides are also used in diagnostics as expressed sequence tags for indentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
2291 AGGITGICGAGACGICTCTCTTGCTTTCTCTCATACATTCTTAGCATAGICCTCATG 2232
                                                                             60 ---IleAlaAlaMetLysLeuSer------SerGluSerLysAla 71
                                                                                                                                                                                72 LysIleSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                          2231 GTAATAGTGCCTTGCTCTGAAAGAAAGACTTCAACCCCCAATCCA 2187
                                                                                                                                                                                                                                                                                           -----ThrGluLeuThrThrAlaAlaIleAsnPro 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel human diagnostic protein #9634.
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23-AUG-2000; 2000US-0649167.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fip. wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 6599; 103pp; English.
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                       BP; 1184 A; 745 C; 669 G; 702 T; 0 other;
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                                                           3300
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                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
at.ftp.wipo.int/pub/published_pct_sequences.
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P-PSDB; ABG10804.
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in casponsible for genetic disorders or other traits to assess biodiversity and and activity and and produces theretypes of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LeuTyrValThrAlaThrLeuMetThrAlaPhe-----ThrLeuAlaSerCysAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2471 CTGACATTCTGGGCCCATGCTCCAAGCCTTCTCTGGTTGTTGTCAGACTGCTCGGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LysileSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3300 BP; 1184 A; 745 C; 669 G; 702 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ThrGluLeuThrThrAlaAlaIleAsnPro 101
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                                                                                                                                                                        Claim 1; SEQ ID No 10795; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-048-196-2 (1-134) x AAS74991 (1-3300)
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79.00
40.748
26.678
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91

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2471 CTGACATTCTGGGCCCATGCTCCAAGCCTTCTCTGGGTTGTTGTCAGACTGCTCGGGAGCC 2412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 LysileSerGluThrAlaCysGlyCysValAlaAspLysAlaProGluAlaValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2231 GTAATAGTGCCTTGCTCTGAAAGAAAGAACTTCAACCCCCAATCCA 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 ------ThrGluLeuThrThrAlaAlaIleAsnPro 101
                                                                                                                                                                                                                         45 LysGlnThrCysGlnThrGlnLeuThrGlyHisGlnTyr----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The compliant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in chapmostics, forenaics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                           DNA encoding novel human diagnostic protein #17470.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0540217.
2000US-0649167.
                                                                13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73
P-PSDB; ABG17479.
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                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
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23-AUG-2000;
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AAS81666;
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2591 CTTTCCCTCACATCAACATTGATGGGCTCCATCAGAGTAACCTTTGCAGCAGTTGCATGC 2532 5 LeuTyrValThrAlaThrLeuMetThrAlaPhe-----ThrLeuAlaSerCysAlaSer 22 23 ThrProGluSerAsnProLysAsnSerSerAlaAsnLeuThrThrSerLeuIle----Conservative: Mismatches: Indels: Gaps: US-10-048-196-2 (1-134) x AAS81666 (1-3300) 104 79.00 40.74% 26.67% 11.69%

Query Match:

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